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Result
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length: 2000000000
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   Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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/SIDSI/gcgdata/geneseq/geneseqp-embl/AA1989_DAT:*
/SIDSI/gcgdata/geneseq/geneseqp-embl/AA1990_DAT:*
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Copyright (c) 1993 - 2000 Comp
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AAB875084
AAY76084
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AAB56023
AAB522637
AAB42329
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             Human protein SEQ
Human full-length
Human contig polyp
Membrane-bound pro
Human PRO1106 Ho
Human PRO1106 UNQ
Murine ADP/ATP tra
Skin cell protein,
Novel human diagno
Human ORFX ORF2093
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369	380.5	382.5	410.5	412	417	32.	432.5	445	446	446	446	446	454.5	454.5	454.5	455.5	479	505.5	508	508	508	521	632	761	800.5	841	902	910	910	1037	1143	1143	1241
14.9	15.3	15.4	16.5	16.6	16.8	17.4	17.4	17.9	•	•	•	•	•	18.3	•	18.4	19.3	20.4	•	•	20.5	•	•	•	•	33.9	•	36.7	•		ა	<u>ه</u>	50.0
323	267	273	377	266	198	316	316	291	411	411	392	392	384	381	289	415	138	166	332	330	241	352	169	208	226	182	370	312	312	292	244	244	461
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AAM41427	AAG29258	AAG29006	ABB60506	AAG28435	AAG12159	AAG49412	AAG11516	AAG30071	AAG49410	AAG11514	AAG49411	AAG11515	AAG29256	AAG29257	AAY31936	AAG29005	ABG22634	AAB42319	AAG28433	AAG28434	AAG12158	AAG30070	AAB50389	AAM93247	AAM41858	аам80061	ABB71306	AAB55903	AAY75964	AAB50388	AAU19941		AAG65800
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ALIGNMENTS

RESULT AAM79077

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AAM79077 standard; Protein; 477

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AAM79077;

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03-FEB-2000;
27-APR-2000;
20-JUN-2000;
19-JUL-2000;
01-SEP-2000;
15-SEP-2000;
20-OCT-2000;
                                                                                                                                                                                                   Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; humanomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation.
                                                                                                                                          09-AUG-2001.
                                                                                                                                                                                                                                                      Human protein SEQ ID NO 1739.
                                                                                                                                                                                                                                                                          06-NOV-2001 (first entry)
                                                                                                                      05-FEB-2001;
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                                                                                                                                                                                  Homo sapiens.
         (HYSE-)
         HYSEQ
                                                        2000US-0496914.
2000US-0560875.
2000US-0598075.
2000US-0620325.
2000US-0654936.
                                                                                                                      2001WO-US04098
                                      2000US-0663561.
2000US-0693325.
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polypeptide

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RESULT
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Best Local Sin
Matches 475;
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Zhao
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QA,
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                               standard;
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Wang J,
Wejhrman
                               Protein;
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, Zhang J, Ren F, C
n T, Goodrich R;
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from
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Vang ZW;
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Note: Some seque specification, at ftp.wipo.int
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                                                    disorders such as Parkinson's disease, Alzheimer's disease, Huntington's chorea, amyotrophic lateral sclerosis, spinal muscular atrophy and Wernicke disease, inflammatory disorders such as nephritis, Crohn's disease, ischaemia reperfusion injury, shock, sepsis and inflammatory bowel disease. The sequences exhibit activity relating to angiogenesis, cell proliferation, cell differentiation, stem cell growth factor, activin or inhibin. Therefore, they can be used to manipulate stem cells in culture to give rise to neuroepithelial cells that can be used to augment or replace cells damaged by illness, accidental damage or genetic disorders. The sequences may also be used for regeneration of bone, cartilage, tendons and ligaments and in tissue repair and burn healing. Note: Some sequences for this patent did not form part of the printed specification, but were obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                 sequences AAU27676-AAU28019 represent full-length polypeptides and contig polypeptides of the invention. The proteins and their associated DNA sequences are useful for the treatment, diagnosis and prevention of various types of disorder in a mammalian subject such as a human, dog, monkey, mouse, hamster or rat. The disorders include cancers such as leukaemia, lymphoma and neuroblastoma, autoimmune disorders such as multiple sclerosis, connective tissue disease, rheumatoid arthritis, diabetes mellitus, allergic rhinitis, asthma and eczema, nervous system disorders mellitus, allergic rhinitis, asthma and eczema, nervous system
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tang YT,
Xue AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel polypeptides and nucleic acids obtained from cDNA libraries prepared from various human tissues, for diagnosis, treatment of cancer, neurological, inflammatory disorders and for use in array.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-FEB-2000; 2000US-0515126.

18-MAY-2000; 2000US-0577409;

17-JUN-2000; 2000US-0597707,

14-JUL-2000; 2000US-0616807,

19-SEP-2000; 2000US-0664641.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 10;
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T, Wang J,
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, Ma Y, W
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Query Match Best Local

Similarity

62.6%;

Score Pred.

1552.5; DB 22; No. 2.3e-133;

Length

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RESULT AAU27869
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ID AAU27869
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                                                                   28-FEB-2000;
18-MAY-2000;
17-JUN-2000;
14-JUL-2000;
19-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mammal; human; rhesus monkey; baker's yeast; fission yeast; Norway rat; mouse; Chinese hamster; African clawed frog; fruit fly; dog; leukaemia; cancer; lymphoma; neuroblastoma; autoimmune disorder; cell proliferation; nervous system disorder; hiflammatory disorder; cell differentiation; angiogenesis; stem cell growth factor; activin; inhibin; cartilage; burn; genetic disorder; bone regeneration; tendon; ligament; tissue repair;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        cytostatic; antirheumatic; antiarthritic; vulnerary; antiinflammatory; antibacterial; immunosuppressive; vasotropic; antiparkinsonian; neuroprotective; osteopathic; antidiabetic; antiasthmatic; antiallergi
                                                                                                                                                                                                                                                                   07-SEP-2001
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                                                                                                                                                                                                                                                                                                                                                                Synthetic
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2000US-0597707.
2000US-0516807.
2000US-0664641.
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Query Match Best Local Matches

Similarity

62.6%;

Conservative

85;

Score 1552.5; Pred. No. 2.6e 35; Mismatches

6e-133; DB

Indels Length 509;

7;

Gaps

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22;

Sequence

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multiple sclerosis, connective tissue disease, rheumatoid arthritis, disbetes mellitus, allergic rhinitis, asthma and eczema, nervous system disorders such as Parkinson's disease, Alzheimer's disease, Huntington's chorea, amyotrophic lateral sclerosis, spinal muscular atrophy and Wernicke disease, inflammatory disorders such as nephritis, Crohn's disease, ischaemia reperfusion injury, shock, sepsis and inflammatory bowel disease. The sequences exhibit activity relating to angiogenesis, cell proliferation, cell differentiation, stem cell growth factor, activin or inhibin. Therefore, they can be used to manipulate stem cells in culture to give rise to neuroepithelial cells that can be used disorders. The sequences may also be used for regeneration of bone, cartilage, tendons and ligaments and in tissue repair and burn healing.
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Xue AJ,
                                                     cartilage, tendons and ligaments and in tissue repair and burn healing. Note: Some sequences for this patent did not form part of the printed specification, but were obtained in electronic format directly from WIP
                                                                                                                                                                                                                                                                                                                                                                                  DNA sequences are useful for the treatment, diagnosis and prevention various types of disorder in a mammalian subject such as a human, downchey, mouse, hamster or rat. The disorders include cancers such as
                                                                                                                                                                                                                                                                                                                                                                                                                            Sequences AAU27676-AAU28019 represent full-length polypeptides and contig polypeptides of the invention. The proteins and their associated DNA sequences are useful for the treatment, diagnosis and prevention of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      detection
                                                                                                                                                                                                                                                                                                                                                                leukaemia, lymphoma and neuroblastoma, autoimmune disorders such
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim
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                                    ftp.wipo.int/pub/published_pct_sequences
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DB; AAS44769.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10; Page 126-127;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         polypeptides and nucleic acids obtained from cDNA libraries red from various human tissues, for diagnosis, treatment of r, neurological, inflammatory disorders and for use in array
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Wehrman
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T, Wang J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              English.
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Ma Y, Wang
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ang D, Chen
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98US-0088217

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; receptor immunoadhesin; gene mapping.
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31-AUG-1998
31-AUG-1998
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                                                                                                                                                                                                                                                                                                                                                                          sequences have homology with proteins including LDL receptors, TIE ligands and various enzymes. The membrane-bound proteins and receptor molecules are useful as pharmaceutical and diagnostic agents. Receptor immunoadhesins, for instance, can be used as therapeutic agents to block receptor-ligand interactions. The membrane-bound proteins can also be employed for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction. The PRO encoding sequences are useful as hybridization probes, in chromosome and gene mapping and in the generation of antisense RNA and DNA. PRO nucleic acid sequences will also be useful for the preparation of PRO polypeptides, especially by recemblant techniques.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              polynucleotides encoding them. The PRO sequences of the invention we identified based on extracellular domain homology screening. The PRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention provides membrane-bound PRO polypeptides and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                claim
                                                                                                                                                                                                                                                                                                                                            Sequence
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                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                  recombinant techniques.
                                                                                         ATAQTFIYPMEVMKTRLAVGKTGQYSGIYDCAKKILKHEGLGAFYKGYVPNLLGIIPYAG
                                                                                                                                                                                                                                   aiaqssiypmevlktrmalrktgqysgmldcarrilaregvaafykgyvpnmlgiipyag
                                                                                                                                                                 IPDEFTEDEKKSGQWWRQLLAGGIAGAVSRTSTAPLDRLKIMMQVHGSKSDKMNIFGGFR
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IDLAYYELLKSYWLDNFAKDSVNPGVMVLLGCGALSSTCGQLASYPLALVRTRMQAQAML
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12; Fig 206; 822pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENENTECH INC.
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Yuan J;
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98US-0097971
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98US-0097978
98US-0097998
98US-009785
98US-0098014
98US-010634
99US-0115565
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65.8%;
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                                                                                                                                                                                                                                                                                Score 1501; DB 21;
Pred. No. 1.2e-128;
1; Mismatches 72;
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                                                                                                                                                                                                                                                                                                         DB 21;
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                                                                                                                                                                                                                                                                                                         Length 469;
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Query Match Best Local Similarity Matches 275; Conserv

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Score 1501; DI Pred. No. 1.2e 71; Mismatches

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18-FEB-2000;

18-FEB-2000;

22-FEB-2000;

01-MAR-2000;

03-MAR-2000;

25-APR-2000;

22-APR-2000;
                                                                                                                                                                                                                                                                                                                                                                      01-SEP-1999;
15-SEP-1999;
07-DEC-1999;
                                                                                                                                                                                                            Eaton DL,
Grimaldi (
                 The present sequence is a human PRO polypeptide (secreted and transmembrane). The PRO protein, and PRO agonists, PRO antagonists or anti-PRO antibodies are useful for preparation of a medicament useful in the treatment of a condition which is responsive to the PRO protein, agonists, antagonists or anti-PRO antibodies. The PRO protein may also be employed as molecular weight markers for protein electrophoresis. The PRO coding sequence has applications in molecular biology, including use as hybridisation probes, and in chromosome and gene mapping.
                                                                                                                                       Eighty four nucleic acids encoding PRO polypeptides, useful in molecular biology, including use as hybridization probes, and chromosome and gene mapping.
                                                                                                               Claim 12; Fig 58; 278pp; English.
Sequence
                                                                                                                                                                                                                                                                05-JUN-2000;
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J, Gurney AL,
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99US-0170262.
2000US-0175481.
2000WO-US04341.
2000WO-US04414.
2000WO-US05601.
2000WS-0197202.
2000US-0197397.
2000US-019337.
2000US-029832.
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26-JUL-1999
28-JUL-1999
17-AUG-1999
17-AUG-1999
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08-OCT-1999
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16-DEC-1999
16-DEC
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07-JUL-1999;
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                              99US-0143048.
99US-0144758.
99US-0145698.
99US-014522.
99US-0146222.
99US-01831096.
99WO-US21547.
99WO-US21813.
99WO-US28313.
99WO-US28313.
99WO-US28301.
2000WO-US30911.
2000WO-US30911.
2000WO-US0376.
2000WO-US0376.
2000WO-US036841.
2000WO-US04914.
2000WO-US0568841.
2000WO-US056884.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequences, and their fragments, can be used as hybridisation probes, in chromosomal and gene mapping, and in the generation of anti-sense RNA and DNA. They may also be used to produce transgenic animals which are used to develop and screen therapeutically useful reagents. The PRO nucleotide and protein sequence can be used for tissue typing and in treating cancer. Anti-PRO antibodies can be used in diagnostic assays. AAF44270 to AAF44470 represent PCR primers and hybridisation probes use in the isolation of human PRO sequences. AAF44087 to AAF4459 and AAB65154 to AAF85300 represent human PRO polynucleotide and protein sequences given in the exemplification of the present invention.
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N-PSDB;
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Ferrara N,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention describes human secreted and transmembrane PRO proteins. The PRO proteins have cytostatic activity. The PRO proteins can be used for targeted delivery of bioactive molecules, such as toxins, radiolabels or antibodies, that cause cell death. PRO nucleotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
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                                                                                                                 EEKIFTTGDVNKDGKLDFEEFMKYLKDHEKKMKLAFKSLDKNNDGKIEASEIVQSLQTLG 119 ::|| || :||:||:||:|| || ||:||:|| || kgkivqagdkdldgqldfeefvhylqdhekkirlvfkildkndgrldaqeimqslrdlg 111
                                                        QMVKEGGIRSLWRGNGTNVIKIAPETAVKFWAYEQYKKLLTEEGQKIGTFERFISGSMAG
EGSPQLNMYGLFRRIISKEGIPGLYRGITPNFMKVLPAVGISYVYYENMKQTLGVTQK
                                                                                                                                                                                                                                                                                                              LTISEQQAELILQSIDVDGTMTVDWNEWRDYFLFNPVTDIEEIIRFWKHSTGIDIGDSLT 179
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DB; AAF44204.
                                                                                                                                                                              qmireggarslwrgnginvlkiapesaikfmayeqikrlvgsdqetlriherlvagslag
                                                                                                                                                                                                                                                                                                                                                                                                                    275;
                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
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N, Fong S, Gerber H, Gerritsen ME, Goddard A,
i CJ, Gurney AL, Kljavin IJ, Napier MA, Pan J,
Stewart TA, Tumas D, Watanabe CK, Williams PM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fig 206; 935pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           469
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AA;
                                                                                                                                                                                                                                                                                                                                                                                                                               60.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       to produce polypeptides used to target as toxins, radiolabels or antibodies, targeted cell death -
                                                                                                                                                                                                                                                                                                                                                                                                                    71;
                                                                                                                                                                                                                                                                                                                                                                                                                   Score 1501; DB 22;
Pred. No. 1.2e-128;
1; Mismatches 72;
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PRO nucleotide
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Wood
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Best Local
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                                                                                                                                                                                                                                                                                                                                                            cancer and neurological diseases. The proteins may be used to stimulate the growth and motility of keratinocytes, to inhibit the growth of cancer cells, to modulate angiogenesis and tumour vascularisation, to modulate skin inflammation, to modulate epithelial cell growth and to inhibit binding of HIV-1 to leukocytes. The invention may also be used to treat growth and developmental defects, skin wounds and hair follicle disorders. Sequences ANT5942-Y5613 represent polypeptides encoded by cDNA sequences ART5942-Y5613 represent polypeptides encoded by cDNA sequences ART5942-Y5613 represent polypeptides encoded by cDNA sequences ART5942-Y5947, ART76020-Y76021, ART76094-Y76104 and
                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                    AAY76119 are proteins with an N-terminal signal sequence, indicating that they are secreted. Sequences AAY75986-Y75989, AAY76061-Y76071, AAY76106-Y76109 and AAY76121-Y76122 are proteins with one or more
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim
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09-NOV-1998;
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                                                                                                                   120
                                                                                                                                              52
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           invention relates to novel nucleic acid sequences derived from rat mal papilla, human keratinocytes and neonatal foreskin fibroblasts, mouse embryonic skin, keratinocyte stem cells and transit amplifying 1s. Polypeptides of the invention may be used to treat inflammation,
                                                                                                                                        EEKIFTTGDVNKDGKLDFEEFMKYLKDHEKKMKLAFKSLDKNNDGKIEASEIVQSLQTLG
QMVKEGGIRSLWRGNGTNVIKIAPETAVKFWAYEQYKKLLTEEGQKIGTFERFISGSMAG
                           vpdeftveerqtg \verb|mwwrhlvagggagavsrtctapldrlkvlmqvhasrsnnmcivggft|
                                                                                   vkiseqqaekilksmdkngtmtidwnewrdyhllhpvenipeiilywkhstifdvgenlt
                                                                                                                  LTISEQQAELILQSIDVDGTMTVDWNEWRDYFLFNPVTDIEEIIRFWKHSTGIDIGDSLT
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                                            IPDEFTEDEKKSGQWWRQLLAGGIAGAVSRTSTAPLDRLKIMMQVHGSKSDKMNIFGGFR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   polynucleotides useful for the ling wounds and cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      dermal papilla; keratinocyte; onic skin cell; keratinocyte s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4; Page 199-200; 235pp; English.
                                                                                                                                                                                                                    Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        skin cell; keratinocyte stem cell; transit a
transmembrane; inflammation; cancer; neurolo
sis; tumour vascularisation; growth disorder;
                                                                                                                                                                                                                                                                                469 AA;
                                                                                                                                                                                                        Conservative
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98US-0188930.
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                                                                                                                                                                                                                   60.4%;
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                                                                                                                                                                                                                    Score 1499; DB Pred. No. 1.8e-1
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128;
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EEKIFTTGDVNKDGKLDFEEFMKYLKDHEKKMKLAFKSLDKNNDGKIEASEIVQSLQTLG 119

Query Match Best Local S Matches 274

1 Similarity 274; Conser

Conservative

60.4%;

Score 1499; DI Pred. No. 1.8e 73; Mismatches

DB 22; .8e-128; les 71;

Indels Length

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Gaps

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1499; No. 1

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AAB56023
ID AABS
                                                      The present sequence is a polypeptide which is expressed in mammalian skin cells. The polypeptide is useful for stimulating keratinocyte growth and motility, inhibiting the growth of cancer c modulating angiogenesis, inhibiting angiogenesis and vascularisatio tumours, modulating skin inflammation, stimulating the growth of epithelial cells, inhibiting the binding of human immunodeficiency (HTV)-1 to leukocytes, and treating inflammatory disease, cancer a neurological diseases. The polynucleotide can be used as a marker, the identification of genetic disorders, and for the design of
                                                                                                                                                                                                                                                                                                            New isolated polynucleotide used in the identification disorders and encoding polypeptides used for treating disease, cancer and neurological diseases -
Sequence
                                                                                                                                                                                                                                                                         Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Watson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (GENE-) GENESIS RES & DEV CORP LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14-MAY-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        keratinocyte growth stimulation; cancer; angiogenesis inhibition; inflammation; neurological disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Strachan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cell; cytostatic; antiinflammatory; anti-HIV;
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                                                                                                                                                                                                                                                                    266-267; 352pp; English.
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                                       patterns.
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                                                                                                                                                                                                                                                  diagnostics, forensics, responsible for genetic biodiversity -
and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving
                                                                        The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation pr polymerase chain reaction (PCR) primers, oligomers, and for cand gene mapping, and in recombinant production of (II). The
                                                                                                                                                                                                                                               biodiversity
                                                                                                                                                                                                                                                                      New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31-MAR-2000;
23-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABG22637
                                                                                                                                                                                                  Claim
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supplement; medical imaging; diagnostic; genetic of
supplement; medical imaging; medical i
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Matches 277
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Note: The sequence data for this patent did not appear in the specification, but was obtained in electronic format directly at ftp.wipo.int/pub/published_pct_sequences.
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277; Conserv
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85; Mismatches
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anticonvulsant; osteopathic; antiarthritic; immunosuppressant; ca immunostimulant; thrombolytic; coagulant; vasotropic; antidiabet; hypotensive; dermatological; immunosuppressive; antiinflammatory; antiviral; antibacterial; antifungal; antirheumatic; antithyrold;

Human; open reading frame; ORFX; detection; cytostatic; hepatotropic; vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotectiv anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardia

nootropic; neuroprotective;

antidiabetic;

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antianaemic; gene therapy; cancer; neurodegenerative disorder; osteoa

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02-APR-1999;
05-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  antipsoriatic; antiparkinsonian; noofropic; neuroprotective; osteopathic; anticonvulsant; antiarthritic; immunosuppressant; immunostimulant; cardiant; thrombolytic; coagulant; vascotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antiinflammatory; antibacterial; antiviral; antifungal; antirheumatic; antithyroid; and antianaemic. The sequences can be used for determining the presence of or predisposition to, or preventing or treating pathological conditions associated with an ORFX-associated disorder. The
                                                                                                                                                                                                                                                                                                                    nucleic acids can be used to express ORFX proteins in gene therapy vectors. The proteins and nucleic acids may be used to treat cancer proliferative disorders, neurodegenerative disorders, osteoarthritigraft vs host disease, cardiovascular disease, diabetes mellitus, hypertension, hypothyroidism, cholesterol ester storage, systemic lerythematosus, severe combined immunodeficiency (SCID), AIDS, viral bacterial or fungal infection, malaria, autoimmune disorders, asthmalaries, aplastic anaemia, burns, wounds, bone and cartilage damanocturnal haemoglobinuria, antiinflammatory disease; to enhance coagulation; to inhibit thrombosis; and as a contraceptive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAC74446 to AAC77606 encode the proteins given in AAB40237 to which represent the human ORFX open reading frames 1 to 3161. sequences have activities such as: cytostatic; hepatotropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cholesterol ester storage; systemic lupus erythematosus; infection; severe combined immunodeficiency; malaria; autoimmune disorder; asthma; allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound; bone damage; cartilage damage; antiinflammatory disease; coagulation;
                                                                                                                                                                                                                                                                                         Sequence
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                      LDRLKIMMQVHGSKSDKMNIFGGFRQMVKEGGIRSLWRGNGTNVIKIAPETAVKFWAYEQ
                                                                                       PVTDIEEIIRFWKHSTGIDIGDSLTIPDEFTEDEKKSGQWWRQLLAGGIAGAVSRTSTAP
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nucleic acids and peptides derived from open reading for treating e.g. cancers, proliferative disorders,
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99US-0127636.
99US-0127728.
2000US-0540763.
                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    disorders and cardiovascular disease
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                                                                                                                                                                                                                      56.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5507pp; English.
                                                                                                                                                                                                     63;
                                                                                                                                                                                                     Score 1394; D
Pred. No. 5.6e
63; Mismatches
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                                                                                                                                                                                                                      DB 21;
.6e-119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothyroidism;
                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                     Length
                                                                                                                                                                                                                                                                                                                                                                       disorders, asthma,
                                                                                                                                                                                                                                                                                                                                                                                                                                     osteoarthritis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   to AAB43397,
61. The ORFX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      frame
                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      cancers,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    vulnerary;
                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                   lupus
      182
                                     274
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in gene of the i

invention encoded po

on relates to human nucleic acids (AAI57798-AAI61369) polypeptides (AAM38642-AAM42213) with nootropic,

and

immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as

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RESULT
AAM40072
                                                                                                                                                                          21-JAN-2000;
25-APR-2000;
09-JUL-2000;
19-JUL-2000;
03-AUG-2000;
                                                                                                     Tang
                                                                                                                                                                                                                                                                                                                               Human; nootropic; immunosuppressant; cytostatic; gene therapy; cance peripheral nervous system; nerropathy; central nervous system; Nesten; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                      such
                                                                                  2hao
                                                                                          Wang
                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAM40072
  Example
                                Novel nucleic
                                                                                                                                              29-NOV-2000;
                                                                                                                                                      14-SEP-2000;
19-OCT-2000;
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                                                             2001-442253/47.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         polypeptide
 5;
                     central nervous
                                                    AAI59228
                                                                                                                        HYSEQ
                                                                                 Liu (
Wang 2
Zhou
                                                                                                                                                                                                                                                                                                                                                                                                                                                          standard;
  SEQ
                                                                                                                                                     2000US-0488725.
2000US-0552317.
2000US-0598042.
2000US-0620312.
2000US-0653450.
2000US-0662191.
2000US-0693036.
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1 P,
                                                                                                                                              2000US-0727344
                                                                                                                                                                                                                                        2000WO-US34263
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                                                                                         Asundi V,
Wehrman T,
                                                                                                                                                                                                                                                                                                                                                                                              SEQ
  NO
                                                                                  Goodrich
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 3217;
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                     polypeptides, useful system injuries -
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lu C, Xue
Drmanac R
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eAJ,
RT;
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                               treating disorders
                                                                                          g y,
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                                                                                                    Wang
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YAR PRESENTATION OF STREET
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Best Local
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                                                                                                                                                                                                    antiparkinsonian;
                                                                                                                                                                                                                                            Human membrane transporter polypeptide (MTP).
                                                                                                                                                                                                                                                                                                                            AAG65800 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              specification.
                                       30-MAR-2001; 2001WO-US10395
                                                                                            WO200174854-A2
                                                                                                                                                               antidiabetic;
                                                                                                                                                                            antiarteriosclerotic; antiinflammatory;
                                                                                                                                                                                         neuroleptic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MNIFGGFROMVKEGGIRSLWRGNGTNVIKIAPETAVKFWAYEQYKKLLTEEGQKIGTFER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VQSLQTLGLTISEQQAELILQSIDVDGTMTVDWNEWRDYFLFNPVTDIEEIIRFWKHSTG 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               \verb|mgivggftqmireggarslwrgnginvlkiapesaikfmayeqikrlvgsdqetlriher|
                                                                                                                                                                                                                                                                                                                                                                                               lgvqsr 366
                                                                                                                                                                                                                                                                                                                                                                                                                          LGVTQK 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RMQAQAMLEGSPQLNMVGLFRRIISKEGIPGLYRGITPNFMKVLPAVGISYVVYENMKQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LGIIPYAGIDLAVYELLKSYMLDNFAKDSVNPGVMVLLGCGALSSTCGQLASYPLALVRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       fdvgenltvpdeftveerqtgmwwrhlvagggagavsrtctapldrlkvlmqvhasrsnn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IDIGDSLTIPDEFTEDEKKSGQWWRQLLAGGIAGAVSRTSTAPLDRLKIMMQVHGSKSDK 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                     {\tt rmqaqasiegapevtmsslfkhilrtegafglyrglapnfmkvipavsisyvvyenlkit}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       {\tt lgiipyagidlavyetlknawlqhyavnsadpgvfvllacgtmsstcgqlasyplalvrt}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The sequence data
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        disorders.
                                                                                                                                                                                                      transporter polypeptide;
insonian; anticonvulsant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                       cardiant; vasotropic;
                                                                                                                                                                                                                                                                      (first entry)
            2000US-193549P
                                                                                                                                                              hepatotropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AA;
                                                                                                                                                                                                                                                                                                                             Protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           for this patent did not form part of the printed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61;
                                                                                                                                                               antianginal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 1325; DB 22;
Pred. No. 1.1e-112;
51; Mismatches 62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypotensive; antidepressant; h; tranquilizer; antimigraine; atory; cytostatic; antithyroid;
                                                                                                                                                                                                                  MTP; neuroprotective; nootropic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                               gene therapy;
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                                                                                                                                                                                       anorectic;
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> 184 193 124 133

244

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303

GNGTNVIKIAPETAVKFWAYEQYKKLLTEEGQKIGTFERFISGSMAGATAQTFIYPMEVM mwwkqlvagavagavsrtgtapldrlkvfmqvhasktnrlnifgglrsmvleggirslwr Qy

73 64

SIDVDGTMTVDWNEWRDYFLFNPVTDIEEIIRFWKHSTGIDIGDSLTIPDEFTEDEKKSG

183 192

243 252 В

17

DAEQPTRYETLFQALDRNGDGVVDIGELQEGLRNLGIPLGQD----AEEKIFTTGDVNKD

daerrqrwgrlfeeldsnkdgrvdvhelrqglarlg---ggnpdpgaqqgissegdadpd

63

Query Match Best Local Sim Matches 234;

Local Similarity

50.0%; 56.9%;

Conservative

78;

Score 1241; DB 22; Pred. No. 7.6e-105; 78; Mismatches 87;

Length Indels 12;

Gaps

4.

Sequence

human MTP 461

(clone Fbh32449).

Вb

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CC assays, monitoring clinical trials, pharmacogenetics) and therapeutic and cc prophylactic treatment. MTP nucleic acid and protein molecules are useful cas modulating agents in regulating variety of cellular processes, e.g. cc cellular proliferation, growth, differentiation or migration, immune cc responses, hormonal responses, inter- or intra-cellular communication. CC The MTP molecules provide novel diagnostic targets and therapeutic agents to control transporter-associated disorders, including CNS disorders such cc as cognitive and neurodegenerative disorders, e.g. Alzheimer's disease, cl neuropsychiatric disorders (e.g. hypertension and sleep disorders), cc neuropsychiatric disorders (e.g. hypertension and sleep disorders), cc memory disorders (e.g. ammesia or age-related memory loss), bipolar cc affective neurological disorders (e.g. migrathe and obesity). The MTP cc molecules are also useful for treating cardiac-related disorders (e.g. arteriosclerosis), disorders of the musculoskeletal system such as c paralysis and muscle weakness, cellular proliferation, differentiation cor growth disorders including cancer e.g. carcinoma, sarcoma or leukemia, ct tumor angiogenesis and metastasis, hepatic disorders and hematopoietic and/or myeloproliferative disorders. The molecules are also useful for treating hormonal disorders, such as diabetes mellitus, pituitary c disorders, thyroid, reproductive or fertility disorders, immune disorders compounds the import and export of molecules from cells, e.g. hormones, condulate the import and export of molecules from the cell or facilitate the compartmentalization of the molecules into a sequestered intracellular transport of for the molecules into a sequestered contracellular compounds from the cell or intracellular compounds.
                                                                              intracellular space (e.g. the peroxisome) and modulate transport biological molecules across membranes, e.g. the plasma membrane comembrane of the mitochondrion, peroxisome, lysosome, endoplasmic reticulum, nucleus or the vacque. The present sequence represent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention provides a novel human membrane transporter polypeptide (MTP). The MTP polypeptide can be expressed by standard recombinant methodology. MTP polypeptides, polynucleotides and antibodies are useful in screening assays, predictive medicine (diagnostic assays, prognostic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 13; Fig 1A-B; 114pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         diagnosis, prevention and proliferation, hormonal, i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel human membrane transporter polypeptides and polynucleotides diagnosis, prevention and treatment of central nervous system, ceproliferation, hormonal, immune and cardiac-related disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (MILL-) MILLENNIUM PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 in screening assays,
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DB; AAI66980, AAI66981.
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    18-APR-2000

19-MAY -2000

28-JUN-2000

30-JUN-2000

07-JUL-2000

07-JUL-2000

11-JUL-2000

11-JUL-2000

14-JUL-2000

14-AUG-2000

14-A
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04-FEB-2000;
24-FEB-2000;
02-MAR-2000;
16-MAR-2000;
17-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; antiarthritic; antirheumatic; antiproliferative; vasotropic; cerebroprotective; nootropic; neuroprotective; antibacterial; virucide; fungicide; ophthalmological; cytostatic; immunosuppressive; nootropic; neuroprotective; antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer; vulnerary; anticonvulsant; antibacterial; antiparasitic; cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder; neurological disease; infection; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17-JAN-2001;
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-MAR-2000;
-MAR-2000;
-APR-2000;
-MAY-2000;
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N-2000;
N-2000;
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  2000US-017905.
2000US-0186628.
2000US-0184664.
2000US-0189874.
2000US-0199173.
2000US-0199173.
2000US-0214886.
2000US-0214886.
2000US-0215135.
2000US-0216880.
2000US-0216880.
2000US-0217487.
2000US-0217487.
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2000US-0218290.
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2000US-0224518.
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2000US-0229343.
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17-NOV-2000; 17-NOV-2000; 17-NOV-2000;

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17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
01-DEC-2000;
                                                                                                                                                                                                                    colitis; (c) cardiovascular disorders such as mycardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, funorand parasitic infections.
                                                                                                                                                                                                                                                                                  The invention relates to human polynucleotides (AAI63803-AAI64012) and the encoded proteins (AAM434497-AAM43660) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes were isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative
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05-DEC-2000;
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17-NOV-2000;
                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim
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N-PSDB; AAI63830.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated nucleic acids and
                          61
  74
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                                                 : The sequence data for this patent did not form p
ted specification, but was obtained in electronic
WIPO at ftp.wipo.int/pub/published_pct_sequences.
EKIFTTGDVNKDGKLDFEEFMKYLKDHEKKMKLAFKSLDKNNDGKIEASEIVQSLQTLGL 120
                                                                                                      al Similarity
219; Conserv
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2000US-0249265.
2000US-0249300.
2000US-0250160.
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94.88;
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Pred. No. 2.7e
0; Mismatches
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14-AUG-2000

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16-AUG-2000

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18-AUG-2000

19-AUG-2000

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19-AUG-2000

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10-SEP-2000
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19-MAY-2000;
07-JUN-2000;
28-JUN-2000;
30-JUN-2000;
07-JUL-2000;
07-JUL-2000;
11-JUL-2000;
11-JUL-2000;
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04-FEB-2000;
24-FEB-2000;
02-MAR-2000;
16-MAR-2000;
17-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; calcium-binding protein; calcium flux; neurological disease; immune dysfunction; digestive disorder; neoplastic disease; blood disorder; infectious disease; gene therapy; immunosuppressive; antiarthritic; cytostatic; vasotropic; antibacterial; nootropic;
                                                                                                                                                                                                                                                                                                                                                                                                  17-JAN-2001;
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2000US-0209467.

2000US-0214886.

2000US-0215135.

2000US-0216647.
                                                                          2000US-0225758.
2000US-0225759.
2000US-0226279.
2000US-0226681.
                                                                                                               2000US-0225214.

2000US-0225266.

2000US-0225267.

2000US-0225278.

2000US-0225278.

2000US-02257447.

2000US-0225757.
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2000US-0217487.
2000US-0217496.
2000US-0218290.
2000US-0220963.
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2000US-0224518.
2000US-0224519.
2000US-0225213.
                                               2000US-0226868.
2000US-0227182.
2000US-0227009.
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                            2000US-0228924
2000US-0229287
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2000US-0198123
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05-SEP-2000; 05-SEP-2000; 06-SEP-2000; 06-SEP-2000; 08-SEP-2000;

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Best Local S
Matches 219
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01-DEC-2000;
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N-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim
                                                     121
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nes 219; Conserv
                                                                                                          74
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DB; AAS31626.
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nilarity 94.8%;
Conservative
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2000US-0249245.
2000US-0249265.
2000US-0249265.
2000US-0249299.
2000US-0249299.
2000US-0249299.
2000US-0250316.
2000US-0251030.
2000US-0251030.
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2000US-0251868.
2000US-0251868.
2000US-0251868.
2000US-0251869.
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2.7e-96;
hes 12;
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medical condition
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nosis of diseases
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2000US-0229509
2000US-0229509
2000US-0230439
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2000US-024687

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Matches 181
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08-JUL-1999;
18-AUG-1999;
12-NOV-1999;
                                                                                                                                                                                          The present sequence is a human uncoupling protein. The nucleotide sequences encoding the uncoupling proteins may be used for the detection of various disorders such as cancer, for chromosome identification, as chromosome markers and for numerous other diagnostic or research purposes. The uncoupling protein encoded by the nucleotide sequences may be used to treat disorders such as neural, immune, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal and proliferative disorders, wounds, infectious diseases, thrombosis, arthritis, and infertility.
                                                                                                                                                                                                                                                                                                                                             Uncoupling proteins and nucleic acid sequences encoding them, useful for detecting, preventing and treating proliferative, neurological, immune system, cardiovascular and gastrointestinal disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 antirheumatic; antiproliferative; cardiant; vasotropic; cerebroprotective; neuroprotective, antibacterial; opthalmological; gastrointestinal; nephrotropic; gynaecological; vulnerary; thrombolytic; gene therapy; cancer; wound; infectious disease; thrombosis; arthritis;
                                                                                                                                                                                         thrombosis, arthritis,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human uncoupling protein #11.
                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                       Claim 11; Page 328-329; 343pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-656322/63.
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                                                                            MTVDWNEWRDYFLFNPVTDIEEIIRFWKHSTGIDIGDSLTIPDEFTEDEKKSGQWWRQLL 199
                                                                                                                                                                                                                                                                                                                                                                                                                                      , MS
                                                                                                                   Similarity
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                                                                                                                                                                      292 AA;
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Search completed: August 18, Job time: 3814 sec 2002, 09:22:20 THIS PAGE BLANK (USPTO)

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Result
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sequence
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SIYE	2 QMIREGGAKS 0 ATAQTFIYPM :	172 VPDEFTVEER 240 QMVKEGGIRS		IS KI	Query Match Best Local Similarity Matches 274; Conser	RESULT 1 US-09-188-930-339 Sequence 339, Application US/091 Patent No. 6150502 GENERAL INFORMATION: APPLICANT: Watson, James D. APPLICANT: Strachan, Lorna APPLICANT: Sleeman, Matthew APPLICANT: Murison, James Greg TITLE OF INVENTION: Composition TITLE OF INVENTION: Composition TITLE OF INVENTION: Mand Methods FILE REFERENCE: 11000.1011c1 CURRENT APPLICATION NUMBER: US/ CURRENT APPLICATION NUMBER: US/ CURRENT FILING DATE: 1998-11-09 NUMBER OF SEO ID NOS: 348 SOFTWARE: FastSEQ for Windows V SEO ID NO 339 LENGTH: 469 TYPE: PRT ORGANISM: Mouse US-09-188-930-339		35 198.5 8.0 36 198.5 8.0 37 193.5 7.8 38 193.5 7.8 39 193.5 7.8 40 186 7.2 41 179 7.2 42 179 7.2 44 179 7.2 44 179 7.2 45 178 7.2	4 198.5 8.
SGMLDCARRILAKEC VMVLLGCGALSSTCC	SLWRGNGINVLKIAPESAIKFMAYEQMKRLVGSDQ MEVMKTRLAVGKTGQYSGIYDCAKKILKHEGLGAF : : :	AVS	: : : SMDKNGTMTIDWNEWR)WWRQLLAGGIAGAVS	(LDFEEFMKYLKDHEKKMKLAFKSLD 	60.4%; Score 1499; DB 4; 65.6%; Pred. No. 5.5e-138 vative 73; Mismatches 71	James D. , Lorna Matthew Matthew James Greg Compositions Isolated From Sk and Methods For Their Use 10.1011c1 NUMBER: US/09/188,930A 11.09 13.348 11.09 S: 348 Dr Windows Version 3.0	ALIGNMENTS	303 3 US-09-210-681-37 303 3 US-09-46-712A-37 307 2 US-08-807-861A-56 307 3 US-09-210-681-56 307 3 US-09-223-320 256 2 US-08-905-223-320 256 2 US-08-937-466-6 256 3 US-09-172-528-6 256 4 US-09-318-199-6 256 4 US-09-318-199-6 256 4 US-09-318-199-6 256 4 US-09-503-579-6 149 1 US-08-100-874-2	03 2 US-08-470-1
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SEQ ID NO 142
LENCTH: 312
TYPE: PRT
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Patent No. 6013858
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APPLICANT: Strachan, Lorna
APPLICANT: Sleeman, Matthew
APPLICANT: Onrust, Rene
APPLICANT: Onrust, Rene
TITLE OF INVENTION: Compositions Isolated from Skin Cells
TITLE OF INVENTION: and Methods For Their Use
FILE REFERENCE: 11000.1011c1
CURRENT APPLICATION NUMBER: US/09/188,930A
CURRENT FILING DATE: 1998-11-09
                                                                                                                                                                                                                 GENERAL INFORMATION:
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                              TITLE OF INVENTION: Mouse Lacking Heart-Muscle A
TITLE OF INVENTION: Nucleotide Translocator Prot
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
STREET: 5370 Manhattan Circle, Suite 201
                                                                                                                                                    APPLICANT: Wallace, Douglas C. APPLICANT: Graham, Brett H. APPLICANT: MacGregor, Grant R.
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                                                                                                                                                                                                                                                                              Patent No. 6281409 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                 Sequence 15, Application US/09068140A Patent No. 6281409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 95; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (303) 499-80 INFORMATION FOR SEQ ID NO:
COUNTRY: USA
ZIF: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                      APPLICANT: Mary Rose Woodhead, Mark Andrew Taylor APPLICANT: and Rex Michael Brennan TITLE OF INVENTION: Blackcurrant Promoters and Genumber of SEQUENCES: 15
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 298 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION: TELEPHONE: (303) 499-8080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 01-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: Ferber, Donna M.
REGISTRATION NUMBER: 33,6
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 800 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                      245
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: line
                                                                                                STREET: 709 Swedeland CITY: King of Prussia STATE: PA
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OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/0 FILING DATE: 31-OCT-1997
                                                                                                                                       ADDRESSEE: SmithKline
STREET: 709 Swedeland
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             EGSPQL -- NMVGLFRRIISKEGIPGLYRGITPNFMKVLPAVGISY -- VVYENMKQ 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FIYPMEVNKTRLA--VGKTG---QYSGIYDCAKKILKHEGLGAFYKGYVPNLLGIIPYAG 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AYFGVYDTAK-----GMLPDPKNVHIIVSWMIAQSVTAVAGLVSYPFDTVRRRMMQSGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FVYPLDFARTTLAADVGKGSSQREFNGLGDCLTKIFKSDGLKGLYQGFSVSVQGIIIYRA 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDRHKQFWRYFAGNLASGGAAGATSLC 129
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SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                Blackcurrant Promoters and Genes: 15
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US-09-068-140A-10
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; Patent No. 6281409
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                                                                                                                                                                             GENERAL INFORMATION:
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                          TITLE OF INVENTION: Blackcurrant Promoters and Genes NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FRAGMENT TYPE: ORIGINAL SOURCE: ORGANISM: Rib
                                                                                                                                           APPLICANT: Mary Rose Woodhead, Mark Andrew Taylor APPLICANT: and Rex Michael Brennan
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ANTI-SENSE: NO
TYPE: N-terminal
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FILING DATE: No. 6281409ember 4, 1996
ATTORNEY/AGENT INFORMATION:
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PRIOR APPLICATION NUMBER: PCT/EP96/04807
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APPLICATION NUMBER: US/09/068,140A
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                                                                                                                                                                                                                                                                                                                                             424 QLNMVGLFRRIISKEGIPGLYRGITPNFMKVLPAVGISYVVYENMK 469
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REGISTRATION NUMBER: 33,680
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STRANDEDNESS: uni
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COUNTRY:
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                                                                                                                                                                                                                                                                                                             IQDVIG---SIVKKNGYVGLMRGWIPRMLFHAPAAAICWSTYEASK 312
                                                                                                                                                                                                                                                                                                                                                                                                      KSYWLDNEAKDSVNPGVMVLLGCGALSSTCGQLASYPLALVRTRMQAQAM-----LEGSP 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                        MDVVKQRLQL-QSSPYKGVVDCVRRVLVEEGIGAFYASYRTTVVMNAPFTAVHFATYEAT 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GLYRGIGAMGLGAGPAHAVYFSVYEMCKETFS-HGDPSNSGAHAVSGVFATVASDAVITP 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SLWRGNGTNVIKIAPETAVKFWAYEQYKKLLTEEGQKIGTFERFISGSMAGATAQTFIYP 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QFWQFMIAGSIAGSIEHMAMYPVDTLKTRIQGIGSCSAQS---AGLRQALGSILKVEGPA 91
                                                                                                                                                                                                                                                                                                                                                                                 KKGLLEVSPETANDENLLVHATAGAAAGALAAVVTTPLDVVKTQLQCQGVCGCDRFSSSS 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEVMKTRLAVGKTGQYSGIYDCAKKILKHEGLGAFYKGYVPNLLGIIPYAGIDLAVYELL 368
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29.7%;
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n Release #1.0, Version #1.30 (EPO)
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Pred. No. 2.3e-23;
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US-08-933-750C-12

Sequence 12, Application US/08933750C Patent No. 5932442

GENERAL INFORMATION:

APPLICANT: APPLICANT: APPLICANT: APPLICANT:

Lal, Preeti
Hillman, Jennifer L.
Bandman, Olga
Shah, Purvi
Au-Young, Janice
Yue, Henry

RESULT

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US-09-068-140A-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP96/048
FILING DATE: No. 6281409ember 4,
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE
HYPOTHETICAL: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION: TELEPHONE: 610-270-5017
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE:
236
                                    429
                                                                        176
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                                                                                                                                                                                                                                                                                                                            198 LLAGGIAGAVSRTSTAPLDRLKIMMQVHGSKSDKMNIFGGFRQ----MVKEGGIRSLWRG 253
                                                                                                                                                                             314 TRLAVGKTGQYSGIYDCAKKILKHEGLGAFYKGYVPNLLGIIPYAGIDLAVYELLKSYWL
                                                                                                                                                                                                                                                        254
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                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Dinner, Dara L. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                          1 MIAGSIAGSIEHMAMYPVDTLKTRIQAIGSCSAQS---AGLRQALGSILKVEGPAGLYRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 289 amino acids
G---SIVKKNGYVGLMRGWIPRMLFHAPAAAICWSTYEASK 273
                                GLFRRIISKEGIPGLYRGITPNFMKVLPAVGISYVVYENMK 469
                                                                  EVSPETANDENLLVHATAGAAAGALAAVVTTPLDVVKTQLQCQGVCGCDRFSSSSIQDVI
                                                                                                       DNFAKDSVNPGVMVLLGCGALSSTCGQLASYPLALVRTRMQAQAM~~~~~LEGSPQLNMV
                                                                                                                                                                                                                                                      NGTNVIKIAPETAVKFWAYEQYKKLLTEEGQKIGTFERFISGSMAGATAQTFIYPMEVMK 313
                                                                                                                                             QRLQL-QSSPYKGVVDCVRRVLVEEGIGAFYASYRTTVVMNAPFTAVHFATYEATKKGLL
                                                                                                                                                                                                                   IGAMGLGAGPAHAVYFSVYEMCKETFS-HGDPSNSGAHAVSGVFATVASDAVITPMDVVK
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YES
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                                                                                                                                                                                                                                                                                                                                                                                    12.6%; Score 311.5; 29.5%; Pred. No. 2.8
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                                                                                                                                                                                                                                                                                                                                                                                      No. 2.8e-22;
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                                                                                                                                                                                                                                                                                                                                                                                                   DB 4;
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IMMEDIATE SOURCE:
LIBRARY: SPLNNOT02
CLONE: 207452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Diskette
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APPLICANT: Corley, Neil C.
TITLE OF INVENTION: HUMAN R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS
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300 FFSYE 304
                                                                                240
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                                      462 YVVYE 466
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      187 DEKKSGQ---WWRQLLAGGIAGAVSRTSTAPLDRLKIMMQVHG---SKSDKMNIFGGF-- 238
                                                                                                                                                                                                                                                                                                                                             65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM:
SOFTWARE: FastSEC
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                                                                                FKKRLQVGGFEHARAAFGQVRRYKGLMDCAKQVLQKEGALGFFKGLSPSLLKAALSTGFM 299
                                                                                                                                                                     TLIAIFPYAGLQFSCYSSLKHLYKWAIPAEGKKNENLQNLL-CGSGAGVISKTLTYPLDL
                                                                                                                                                                                                             NLLGIIPYAGIDLAVYELLKS-YWLDNFAKDSVNPGVMVLLGCGALSSTCGQLASYPLAL 408
                                                                                                                                                                                                                                                                                                RFISGSMAGATAQTFIYPMEVMKTRLAV-GKTGQYSGIYDCAKKILKHEGLGAFYKGYVP 349
                                                                                                                                                                                                                                                                                                                                             ASRQILQEEGPTAFWKGHVPAQILSIGYGAVQFLSFE----MLTELVHRGSVYDAREFSV 120
                                                                                                                        VRTRMQAQAMLEGSPQLNMV----GLF---RRIISKEGIPGLYRGITPNFMKVLPAVGIS 461
                                                                                                                                                                                                                                                                                                                                                                                                                              DPKPDGRNNTKFQVAVAGSVSGLVTRALISPFDVIKIRFQLQHERLSRSDPSAKYHGILQ 64
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Pred. No. 1.4e-20;
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US-09-234-613-12
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: September 2.
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Guegler, Karl J.
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: HUMAN RI
NUMBER OF SEQUENCES: 98
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IMMEDIATE SOURCE:
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                                 350 NLLGTIPYAGIDLAVYELLKS-YWLDNFAKDSVNPGVMVLLGCGALSSTCGQLASYPLAL 408
                                                                   121
                                                                                                   291 RFISGSMAGATAQTFIYPMEVMKTRLAV-GKTGQYSGIYDCAKKILKHEGLGAFYKGYVP 349
                                                                                                                                                                      239 --RQMVKEGGIRSLWRGNGTNVIKIAPETAVKFWAYEQYKKLLTEEGQKIGTFE----- 290
                                                                                                                                                                                                                                        187 DEKKSGQ----WWRQLLAGGIAGAVSRTSTAPLDRLKIMMQVHG---SKSDKMNIFGGF--
                                                                                                                                      65
                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: sin
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TLIAIFPYAGLQFSCYSSLKHLYKWAIPAEGKKNENLQNLL-CGSGAGVISKTLTYPLDL
                                                                   HFVCGGLAACMATLTVHPVDVLRTRFAAQGEPKVYNTLRHAVGTMYRSEGPQVFYKGLAP 180
                                                                                                                                      ASRQILQEEGPTAFWKGHVPAQILSIGYGAVQFLSFE----MLTELVHRGSVYDAREFSV 120
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o. 6132973
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Bandman, Olga
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27.5%;
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                                                                                                                                                                                                                                                                         Score 295; DB 4;
Pred. No. 1.4e-20;
61; Mismatches 130
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CURRENT APPLICATION NUMBER: US/09/160,119A
CURRENT FILING DATE: 1998-09-24
EARLIER APPLICATION NUMBER: EP 97402511.6
EARLIER FILING DATE: 1997-10-23
EARLIER FILING DATE: 1998-07-02
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 2
LENGTH: 674
TYPE: PRT
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Patent No. 6316219
GENERAL INFORMATION:
APPLICANT: KRIEF, STEPHANE
APPLICANT: SOUCHEF, MICHEL
APPLICANT: BRIL, ANTOINE
TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GH-30985
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Best Local Similarity
Matches 121; Conserv
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                             FRRIISKEGIPGLYRGITPNFMKVLPAVGISYVVYENMKQ 470
                                                                                                                                                                                    LLPQLLGVAPEKAIKLTVNDFVRDKFMHKDGSVPLAAEILAGGCAGGSQVIFTNPLEIVK
                                                                                                                                                                                                                                                  LGSVAGAVGATAVYPIDLVKTRMQNQRSTGSFVGELMYKNSFDCFKKVLRYEGFFGLYRG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FQLFDKAGKGEVTFEDVKQVFGQTTIHQHIPFNWDSE---FVQLHFGKERKRHLTYAEFT 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FQALDRNGDGVVDIGELQE--GLRNL--GIPLGQDAEEKIFTTGDVNKDGK--LDFEEFM
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                                                            --SFANEDGQVSPGSLLL--AGAIAGMPAASLVTPADVIKTRLQVAARAGQTTYSGVIDC
                                                                                         LDNFAKD--SVNPGVMVLLGCGALSSTCGQLASYPLALVRTRMQAQAMLEGSPQLNMVGL
                                                                                                                         IRLQV--AGEITTGPRVSALSVVRDLGFFGIYKGAKACFLRDIPFSAIYFPCYAHVKA--
                                                                                                                                                                                                                   NGTNVIKIAPETAVKFWAYEQYKKLLTEEGQKIGTFERFISGSMAGATAQTFIYPMEVMK
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US-08-933-750C-19

Sequence 19, Applicat Patent No. 5932442 GENERAL INFORMATION: Applicant: Lal, P

9, Application US/08933750C 5932442

APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:

Lal, Preeti Hillman, Jennifer Bandman, Olga

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APPLICANT: APPLICANT:

Shah, Purvi Au-Young, Janice Yue, Henry Guegler, Karl J. Corley, Neil C.

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US-09-160-119-4
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SEQ ID NO 4
LENGTH: 447
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/160,119A CURRENT FILING DATE: 1998-09-24 EARLIER APPLICATION NUMBER: EP 97402511.6 EARLIER FILING DATE: 1997-10-23 EARLIER APPLICATION NUMBER: EP 98401655.0 EARLIER FILING DATE: 1998-07-02 NUMBER OF SEQ ID NOS: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: SOUCHET, MICHEL
APPLICANT: BRIL, ANTOINE.
TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GH-30985
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                                                                                      286
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                                                                                                                                                                                                        KTGQY-SGIYDCAKKILKHEGLGAFYKGYVPNLLGIIPYAGIDLAVYELLKSYWLDNFAK 378
                                                                                                                                                                                                                                                                                    KIAPETAVKFWAYEQYKKLLTEEGQKIGTFERFISGSMAGATAQTFIYPMEVMKTRLAVG
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                                        KEGIPGLYRGITPNFMKVLPAVGISYVVYENMKQ 470
                                                                                                                            D--SVNPGVMVLLGCGALSSTCGQLASYPLALVRTRMQAQAMLEGSPQLNMVGLFRRIIS
                                                                                                                                                                       -AGEITTGPRVSALSVVRDLGFFGIYKGAKACFLRDIPFSAIYFPCYAHVKA----SFAN
                                                                                                                                                                                                                                                         GVAPEKAIKLTVNDFVRDKFMHKDGSVPLAAEILAGGCAGGSQVIFTNPLEIVKIRLQV-
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EEGPKALWKGAGARVFRSSPQFGVTLLTYELLQR
                                                                                  EDGQVSPGSLLL---AGAIAGMPAASLVTPADVIKTRLQVAARAGQTTYSGVIDCFRKILR
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US-09-234-613-19
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Sequence 19, Application US/09234613
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Best Local S
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SEQUENCE CHARACTERISTICS:
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LIBRARY: SYNOOAT01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: 415-855-0555
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CORRESPONDENCE ADDRESS
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                                                                                             309
                                                                                                                              441 PGLYRGITPNFMKVLPAVGISYVVYE-----NMKQTLG 473
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                                                                                                                                                                                                                                         192 GACVRTAVAQGGWRSLWLGWGPTALRDVPFSALYWFNYELVKS-WLNGLRPKDQTSVGMS 250
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              13 QQMVASGTGAVVTSLFMTPLDVVKVRLQSQRPSMASELMPSSRLWSLSYTKWKCLLYCNG
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nes 79; Conserv
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TOPOLOGY: li
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SOFTWARE: FastSEQ for Windows Version
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CLONE: 724157
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TYPE: amino acid
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                                                                                                                                                                                                    VLLGCGALSSTCGQLASYPLALVRTRMQAQAMLEGSPQLNMVG-----LFRRIISKEGI 440
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                                                                                                                                                                FV--AGGISGTVAAVLTLPFDVVKTQRQVALGAMEAVRVNPLHVDSTWLLLRRIRAESGT
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                                                                                         KGLFAGFLPRIIKAAPSCAIMISTYEFGKSFFQRLNQDRLLG
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ber 23, 1997
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Best Local S
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GENERAL INFORMATION:
APPLICANT: Lal, P
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SEQUENCE CHARACTERISTICS:
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APPLICATION NUMBER: US/08
FILING DATE: September 2:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
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SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Diskett
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APPLICANT: Corley, Neil C.
TITLE OF INVENTION: HUMAN RI
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APPLICANT:
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387 VILIGCGALSSTCGQLASYPLALVRTRMQAQAMLEGSPQLNMVG-----LFRRIISKEGI 440 : | :| | : | : | : | | | | :: |
                                                        192 GACVRTAVAQGGWRSLWLGWGPTALRDVPFSALYWFNYELVKS-WLNGLRPKDQTSVGMS 250
                                                                                                                                133 YFTAYDQLKAFLCGRALTSDLYAPMVAGALARLGTVTVISPLELMRTKLQAQHV-SYREL 191
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                                                                                                                                                                                                                                                                                                                      196 RQLLAGGIAGAVSRTSTAPLDRLKIMMQ------ 223
                                                                                                                                                                     268 KFWAYEQYKKLLTEEGQKIGTFERFISGSMAGATAQTFIYPMEVMKTRLAVGKTGQYSGI 327
                                                                                                                                                                                                           73 VLEPLYLCPNGARCATWFQDPTRFTGTMDAFVKIVRHEGTRTLWSGLPATLVMTVPATAI 132
                                                                                                                                                                                                                                                                                                                                                                           Match 10.3%; Score 255; DB 4; Local Similarity 23.1%; Pred. No. 1.3e-16;
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CLONE: 724157
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STATE: CA
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                                                                                                                                                                                                                                              -----VHGSK-----SDKMNIFG---GFRQMVKEGGIRSLWRGNGTNVIKIAPETAV 267
                                                                                                                                                                                                                                                                                     QQMVASGTGAVVTSLFMTPLDVVKVRLQSQRPSMASELMPSSRLWSLSYTKWKCLLYCNG 72
                                                                                         YDCAKKILKHEGLGAFYKGYVPNLLGIIPYAGIDLAVYELLKSYWLDNF-AKDSVNPGVM 386
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Bandman, Olga
                                                                                                                                                                                                                                                                                                                                                           Conservative
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INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
SEQUENCE STANDARD ACIDS
TENGTH: 311 amino acids
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Best Local 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/775,009
FILING DATE: 27-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION: TELEPHONE: (215) 568-3100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Trujillo, Doreen Yatko
REGISTRATION NUMBER: 35,719
REFERENCE/DOCKET NUMBER: CH-0681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz
ADDRESSEE: No. 5935783ris, LLP
STREET: One Liberty Place - 46th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: No. 5935783el Genes mapping in the Digeorge and TITLE OF INVENTION: vellocardiofacial Syndrome Minimal Critical Region
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                                                                                    147
                                                                                                                                                                                                                                                                                                196 RQLLAGGIAGAVSRTSTAPLDRLKIMMQV-HGSKSDKMNIFGG-FRQMVKEGGIRSLWRG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Roe,
                                    370 SYWLDNFAKDSVNP---GVMVLLGCGALSSTCGQLASYPLALVRTRMQAQAMLEGSPQLN
                                                                                                                                                                                                          254 NGTNVIKIAPETAVKFWAYEQYKKLLTEEGQKIGTFERFISGSMAG-ATAQTFIYPMEVM 312
                                                                                                                                                                        87
                                                                                                                                                                                                                                                        27 KAILAGGLAGGIEICITFPTEYVKTQLQLDERSHPPRYRGIGDCVRQTVRSHGVLGLYRG
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TOPOLOGY: li
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                                                                                                                                                                                                                                                                                                                                                                     Local
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                                                                                                                                                                   LSSLLYGSIPKAAVRFGMFEFLSNHMRDAQGRLDSTRGLLCGLGAGVAEAVVVVVCPMETV 146
                                                                                                                        KTRLAVGKTG---QYSGIYDCAKKILKHEGLGAFYKGYVPNLLGIIPYAGIDLAVYELLK 369
NWYRGDNPNKPMNPLITGVF-----GAIAGAASVFGNTPLDVIKTRMQG----LEAHKYRN
                                                                               KVKFIHDQTSPNPKYRGFFHGVREIVREQGLKGTYQGLTATVLKQGSNQAIRFFVMTSLR
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TR PT
                                                                                                                                                                                                                                                                                                                                            h 9.7%; Score 239.5; DB 2; Similarity 25.4%; Pred. No. 3.5e-15; 74; Conservative 58; Mismatches 142;
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Best Local Similarity
Thes 75; Conserve
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TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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                                                                       184
                                                                                                        362
                                                                                                                                        126 PTDVVKVRFQAQARAGGGRRYQSTVNAYKTIAREEGFRGLWKGTSPNVARNAIVNCA--E 183
                                                                                                                                                                                                                                               248 RSLWRGNGTNVIKIAPETAVKFWAYEQYKKLLTEEGQKIGTFERFISGSMAGATAQTFIY 307
                                                                                                                                                                                                                                                                                                                      197 QLLAGGIAGAVSRTSTAPLDRLKIMMQVHGSKSDKM-----NIFGGFRQMVKEGGI 247
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 240 YSSAGHCALTM-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM:
SOFTWARE: PatentI
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STATE: New Yor
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                                 ----GSPQLNMVGLFRRIISKEGIPGLYRGITPNFMKVLPAVGISYVVYENMKQTL 472
                                                                                         LAVYELLKSYWLD-NFAKDSVNPGVMVLLGCGALSSTCGQLASYPLALVRTRMQAQAMLE
                                                                   LVTYDLIKDALLKANLMTDDLPCHFTSAFGAG----FCTTVIASPVDVVKTRYMNSALGQ
                                                                                                                                                                            PMEVMKTRL-AVGKTG---QYSGIYDCAKKILKHEGLGAFYKGYVPNLL--GIIPYAGID 361
                                                                                                                                                                                                                                                                                     KFLGAGTAACIADLITFPLDTAKVRLQIQGESQGPVRATVSAQYRGVMGTILTMVRTEGP 65
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                                                                                                                                                                                                             RSLYNGLVAGLQRQMSFASVRIGLYDSVKQFYTKGSEHASIGSRLLAGSTTGALAVAVAQ 125
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(212) 869-9741/8864
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VENTION: COMPOSITIONS AND METHODS FOR THE
VENTION: TREATMENT OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     unknown
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SYSTEM: PC-DOS/MS-DOS
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-LQKEGPRAFYKGFMPSFLRLGSWNVVMFVTYEQLKRAL
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Pred. No. 1.3e-14;
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RESULT

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RESULT 15
US-08-518-878B-51
; Sequence 51, Application US/08518878B
; Patent No. 5702902
; GENERAL INFORMATION:
; APPLICANT: Tartaglia, Louis A.
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Best Local Similarity 25.3%;
Matches 75; Conservative 50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: COTUZZI, LAUTA A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7853-0031-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEPAX: (212) 869-8864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Tartaglia, Louis C.
TITLE OF INVENTION: Compositions and Methods for the
TITLE OF INVENTION: Treatment of Body Weight Disorders,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                   421
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                                                                                                                                                                                                                                                    184 LVTYDLIKDALLKANLMTDDLPCHFTSAFGAG----FCTTVIASPVDVVKTRYMNSALGQ
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/0 FILING DATE: 06-JUN-1995
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5. 5861485
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Pred. No. 1.3
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                  AND METHODS
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MEDIUM TYPE: Floppy disk
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TELEFAX: (212) 869-
TELEX: 66141 PENNIE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
                                                                                                                                                                                                                                                                                                   16 KFLGAGTAACIADLITFPLDTAKVRLQIQGESQGPVRATVSAQYRGVMGTILTMVRTEGP 75
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                                     ----GSPQLNMVGLFRRIISKEGIPGLYRGITPNFMKVLPAVGISYVVYENMKQTL 472
                                                                                              LAVYELLKSYMLD-NFAKDSVNPGVMVLLGCGALSSTCGQLASYPLALVRTRMQAQAMLE 420
                                                                                                                                                                                PMEVMKTRL-AVGKTG---QYSGIYDCAKKILKHEGLGAFYKGYVPNLL--GIIPYAGID 361
YSSAGHCALTM-----LQKEGPRAFYKGFMPSFLRLGSWNVVMFVTYEQLKRAL
                                                                          LVTYDLIKDALLKANLMTDDLPCHFTSAFGAG----FCTTVIASPVDVVKTRYMNSALGQ
                                                                                                                                                    PTDVVKVRFQAQARAGGGRRYQSTVNAYKTIAREEGFRGLWKGTSPNVARNAIVNCA--E
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(212) 869-9741/8864
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hypothetical protein F55All.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T22688
R;Kershaw, J.
R;Kershaw, J.
R;Mershaw, J.
R;Accession: T22688
A;Reference number: Z19600
A;Accession: T22688
A;Accession: T22688
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-588 <WIL>
A;Cross_references: EMBL: Z72511; pIDN:CAA96658.1; GSPDB:GN00023; CESP:F55All
A;Cross_references: EMBL: Z72511; pIDN:CAA96658.1; GSPDB:GN00023; CESP:F55All
protein F17E5.2 [imported] - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text C;Accession: G89667 R;anonymous, The C. elegans Sequencing Consortium. Science 282, 2012-2018, 1998 A;Title: Genome sequence of the nematode C. elegans: a pA;Title: Genome sequence wustl.edu/gsc/C_elegans/ and A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and A;Note: published errata appeared in Science 283, 35, 19
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A;Map position: X
A;Introns: 21/1; 48/3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QVPEDFTPQELLSGVWWRHLVAGGVAGAMSRTCTAPFDRIKVYLQVMYLHLLFHIMFLKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QSGSSSVNLNEFQDFMLLYPSTDMRDMVDFWRHNLVCTCLESNSRFRTQNFQIIDIGEDG 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QNISRLSRIRDMYDRLDADNDGSIDIRDLTQAL-SLQAHIPASVAPKLLERMKSEHSDRV 69
      EQPTRYETLFQALDRNGDGVVDIGELQEGLRNLGIPLGQDAEEKIFTTGDVNKDGKLDFE 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GIKCFYKGYLPNLLGIIPYAGIDLTVYESLKSMY-TKYYTEHTEPGVLALLACGTCSSTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           --EGQKIGTFERFISGSMAGATAQTFIYPMEVMKTRLAVGKTGQY-SGIYDCAKKILKHE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYADFTNYVIAHEARLAEVFDKIDLNSDGEVDMAEIKSYCKEMGVNLDDQKAMSIVKKMD 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DFEEFMKYLKDHEKKMKLAFKSLDKNNDGKIEASEIVQSLQTLGLTISEQQAELILQSID 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LQVNSTKTNKLGVVSCVHLLHAEGGIKSFWRGNGINVIKIAPESAMKFMCYDQIKRWMQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VDGTMTVDWNEWRDYFLFNPVTDIEEIIRFWKHSTG------IDIGDSL 178
                                                                                                                  21/1; 48/3;
                                     202;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  203;
                                                                                                                                                                                                                1-587 <WIL>
                                                     Similarity
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er: Z19368
                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                   EMBL: Z50873;
                                                                                                                  74/2; 111/3; 183/2;
                                                                                                                                                                                   clone
                                                                                                                                                                                                                                                  translated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             40.0%;
                                                     39.8%;
42.3%;
                                                                                                                                                                                                                                                                                               Library,
                                                                                                                                                                                  873; PIDN:CAA90761.2;
F17E5
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                                   91;
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                                     Score 988.5;
Pred. No. 1.4e
91; Mismatches
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Pred. No. 7.7e-58;
2; Mismatches 138;
                                                                                                                                                                                                                                                                                                 August
                                                                                                                                                                                                                                                  GB/EMBL/DDBJ
                                                                                                                    384/1;
                                                     ; DB 2
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                                      137;
                                                                                                                     432/3;
                                                                                                                                                                                                   GSPDB:GN00028;
                                                                                                                                                                                                                                                                                                                                                #text_change
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                                      Indels
                                                                   Length
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                                      47;
                                                                                                                     541/3
                                                                                                                                                                                                    CESP: F17E5
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                                        8
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A; Experimental source: cul
C; Genetics:
A; Gene: ATSP:T211.30
A; Map position: 5
A; Introns: 133/1; 391/1; 4
C; Keywords: peroxisome
                                                                                                                                                                                                                                                                                                                                                                                                                                   peroxisomal Ca-dependent solute carrier-like protein - Arabidopsis thaliana NyAlternate names: protein T2II.30
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 09-Jun-2000 C;Accession: T49871
R;Bevan, M.; Murphy, G.; Ridley, P.; Hudson, S.; Bancroft, I.; Mewes, H.W.; submitted to the Protein Sequence Database, April 2000
A;Reference number: Z24493
A;Accession: T49871
A;Status: preliminary
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A; Residues: 1-479 <BEV>
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Best Local Similarity
Matches 181; Conserv
                 198
                                               153
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                                         TMTVDWNEWRDYFLFNP-VTDIEEIIRFWKHSTGIDIGDSLTIPDEFTEDEKKSGQWWRQ
              LLAGGIAGAVSRTSTAPLDRLKIMMQVHGSKSDKMNIFGGFRQMVKEGGIRSLWRGNGTN
                                                                                                      EFRRYIDAKELELYRIFQAIDVEHNGCILPEELWEALVKAGIEIDDEELARFVEHVDKDN
                                                                                                                                  EFMKYLKDHEKKMKLAFKSLDKNNDGKIEASEIVQSLQTLGLTISEQQAELILQSIDVDG
                                                                                                                                                                                             EQPTRYETLFQALDRNGDGVVDIGELQEGLRNLGIPLGQDAEEKIFTTGDVNKDGKLDFE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CFYKGYLPNLLGIIPYAGIDLTYYESLKSMY-TKYYTEHTEPGYLALLACGTCSSTCGQL
                                                                                                                                                                EREIRIRSLFDFFDNSNLGFLDYAQIEKGLASLQIPPEYKYARDLFRVCDANRDGRVDYQ 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AFYKGYVPNLLGIIPYAGIDLAVYELLKSYMLDNFAKDSVNPGVMYLLGCGALSSTCGQL 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DEFTEDEKKSGQWWRQLLAGGIAGAVSRTSTAPLDRLKI---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GAELSTIERLLAGSSAGAISQTAIYPMEVMKTRLALRRTGQLDKGMFHFAHKMYTKEGIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GQKIGTFERFISGSMAGATAQTFIYPMEVMKTRLAVGKTGQY-SGIYDCAKKILKHEGLG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TMTVDWNEWRDYFLFNPVTDIEEIIRFWKHSTG------
EDFTPQELLSGVWWRHLVAGGVAGAMSRTCTAPFDRIKVYLQVMYLHLLFHIMFLKALQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SSSVNLNEFQDFMLLYPSTDMRDMVDFWRHNLVCTCLESNSRFRTQNFQIIDIGEDGQVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DFTNYVIAHEARLAEVFDKIDLNSDGEVDMAEIKSYCKEMGVNLDDQKAMSIVKKMDQSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EFMKYLKDHEKKMKLAFKSLDKNNDGKIEASEIVQSLQTLGLTISEQQAELILQSIDVDG
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                                                                                                                                                                                                                                                                                                                     421/2
                                                                                                                                                                                                                                           34.3%;
                                                                                                                                                                                                                              90;
                                                                                                                                                                                                                           Score 852; DB 2; I
Pred. No. 1.1e-48;
0; Mismatches 172;
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                                                                                                                                                                                                                                                       Length 479,
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mitochondrial solute carrier protein homolog - Arabidopsis thaliana N;Alternate names: protein A_IG002N01.16 C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 19-reb-1999 #sequence_revision 19-Feb-1999 #text_change 24-Nov-1999 C;Accession: T01729
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C; Keywords:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: EMBL:AF007269; NID:g2191126; PID:g2191150 A;Experimental source: cultivar Columbia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-352 <SCH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     submitted to the EMBL Data Library, June 1997
A;Description: The sequence of A. thaliana IG002N01
A;Reference number: Z14407
A;Accession: T01729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Accession: T01729
R; Scheet, P.; Maggi, L.
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Best Local :
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 334
                                                                                                                                220
                                                                                                                                                364 VYELLKSYWLDNFAKDSVNP-------GVMVLLGCGALSSTCGQLASYPLALVRTRMQ
                                                                                                                                                                                                  160
                                                                                                                                                                                                                                                                 100
                                                                                                                                                                                                                                                                                                  255
                                                                                                                                                                                                                                                                                                                                                   196 RQLLAGGIAGAVSRTSTAPLDRLKIMMQVHGSKSDKMN-IFGGFRQMVKEGGIRSLWRGN 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           440
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nes 115; Conserv
FVTYEMVKDVLGV
                             YVVYENMKQTLGV
                                                            MYGWKDASAIYTGEGRSTASLEYTGMYDAFRKTYRHEGFGALYKGLYPNSYKYYPSIAIA
                                                                                                                                                                                               GTNCARIVPNSAVKEFSYEQASNGILYMYRQRTGNENAQLTPLLRLGAGATAGIIAMSAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----AQAMLEGSPQ------LNMVGLFRRIISKEGIPGLYRGITPNFMKVLPAVGIS
                                                                                                                               VYESLKD-WL---VKE--NPYGLVENNELTVVTRLTCGAIAGTVGQTIAYPLDVIRRRMQ
                                                                                                                                                                                                                                                                                             GTNVIKIAPETAVKFWAYEQ------YKKLLTEEGQKIGTFERFISGSMAGATAQTFI 306
                                                                                                                                                                                                                                                                                                                              KSLFAGGVAGGVSRTAVAPLERMKILLQVQNPHNIKYSGTVQGLKHIWRTEGLRGLFKGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KGEGLRGFYRGLLPNLLKVVPAASITYIVYEAMKKNMAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ILQDT-EPGPLIQLSCGMTSGALGASCVYPLQVVRTRMQAD----
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                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                             474
                                                                                                                                                                                                                                                                                                                                                                                                                  21.0%; 36.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                  Score 521; DB 2;
Pred. No. 4.9e-27;
                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
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A; Reference number: 224473
A; Accession: 747703
A; Status: preliminary
A; Molecule type.
A;Map position: 3
A;Introns: 98/3; 157/3; 207/3; 234/3; 258/2; 281/1
A;Note: F5K20.240
C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier
                                                                                                                                                                                                                                                                                                                                                              A; Reference number: Z23017
A; Acession: T45934
A; Actession: T45934
A; Care and the control of 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein F5K20.240 - Arabidopsis thaliana (F5K20.240 - Arabidopsis thaliana cress) (F5K20.240 - Arabidopsis thaliana (F5K20.240 - 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT
T45934
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A;Introns: 63/3; 122/3; 172/3; 206/3; 230/2; 253/1
A;Note: FIII6.50
C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ca-dependent solute carrier-like protein - Arabidop W;Alternate names: protein F1116.50 C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 C;Accession: T47703 R;Benes, V.; Wurmbach, E.; Drzonek, H.; Ansorge, W.
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                                                                                                                                                       A; Experimental source: C; Genetics:
                                                                                                                                                                                                                                 A; Residues: 1-358 <MON>
A; Cross-references: EMB
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A; Residues: 1-332 <BEN>
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Pred. No. 5.3e-27;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length
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R;Lyne, M.; Rajandream, M.A.; submitted to the EMBL Data Lil
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A; Residues: 1-500 <LYN>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         96 WIHDTPHMKLVFHRLQNLPDGDLL-----LENDPKNNVGY--FISGGIAGIVSRTCTAP 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SPDB:SPBC12D12.05c
                                                                                     K-SIILSNAKELYKSVGIRGYYRGVLVGILGMFPYSATDLGTFEGLKRTWIGILASRDNV
                                                                                                                                                   QYSGIYDCAKKILKHEGLGAFYKGYVPNLLGIIPYAGIDLAVYELLKSYWLDNFA-KDSV 381
                                                                                                                                                                                                                                                                                                                                                                                                                                    LDRLKIMM-QVHGSKSDKMNIFGGFRQMVK----EGGIRSLWRGNGTNVIKIAPETAVKF 269
                                                                                                                                                                                                                                                                                                           WAYEQYKKLL--TEEGQKIGTFERFISGSMAGATAQTFIYPMEVMKTR-----LAVGKTG 322
       NPGVM-----VLLGCGALSSTCGQLASYPLALVRTRMQAQ-----
                                                                                                                                                                                                                                     GTYEAMKRVLGISSSSENHSPLYSYLAGGMAGSVAQMFIYPVDTLKFRIQCSDLSRGQHG
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35.8%;
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168 HSTGIDIGDSLTIPDEFTEDEKKSGQWWRQ------LLAGGIAGAVSR 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TSTAPLDRLKIMMQVHGSKSD-----KMNIFGGFRQMVKEGGIRSLWRGNGTNVIKIAPE 264
GTFKHIFKTEGMRGLYRGIIPEYYKVVPGVGIAFMTFEELKKLL
                                                                                                                                                                                                                                                                                                                 GAVNFYAYEEYKTFLHSNPVLQSYKGNAGVDISV--HFVSGGLAGLTAASATYPLDLVRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HNTVVDAGNRKLLQQQPQTQQTQSCHQHHQSNKQSLNQQQGHFGTVERLLAGGIAGAFSK 84
                                              GLFRRIISKEGIPGLYRGITPNFMKVLPAVGISYVVYENMKQTL
                                                                                                                                                                                                                                                             RLAVGKTGQYSGIYDCAKKILKHEGLGAFYKGYVPNLLGIIPYAGIDLAVYELLKSYWLD 374
                                                                                                                                                                                                                                                                                                                                            TAVKFWAYEQYKKLLTEE------GKIGTFERFISGSMAGATAQTFIYPMEVMKT 314
                                                                                                                                                      NFAKDSVNPGVMVLLGCGALSSTCGQLASYPLALVRTRMQAQAMLEGSP----
                                                                                                                                                                                                               RLSA-----QGVGHAFRTICREEGILGLYKGLGATLLGVGPSLAISFAAYETFKTFWLS 256
                                                                                                                                                                                                                                                                                                                                                                                                                         TCTAPLARLTILFQIQGMQSEAAILSSPNIWHEASRIVKEEGFRAFWKGNLVTVAHRLPY 144
                                                                                                       -- NAVVSLGCGSLSGIVSSTATFPLDLVRRRMQ----LEGAGGRARVYTTGLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 506; DB 2;
Pred. No. 4.9e-26;
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                                                                                                                                                           -QLNMV 428
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                                                                                                       309
                                                                                                                                                                                                                                                                                                                      202
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probable mitochondrial carrier protein - fission yeast (Schizosaccharomyces C;Species: Schizosaccharomyces pombe C;Date: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 20-Oct-2000 C;Accession: T39385 A;Cross-references: EMBL:AL035085; PIDN:CAA22679.1; A;Experimental source: strain 972h-; cosmid c12D12 A.; Barrell, B.G.;
Library, January 1 ; Xiang, 1999 z.; GSPDB:GN00067; SPDB:SPBC12D12.05c Aves, pombe)

63;

Mismatches 109;

Indels

Gaps

12;

AMLEGSPQLNMVGL 430

326

267

207

Score 500.5; DB 2 Pred. No. 1.8e-25;

DB 2;

Length

500; 49;

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RESULT
D84798
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                                                                               probable mitochondrial carrier protein [imported] - Arabidopsis
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change
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A;Title: Sequence and pattern of expression A;Reference number: 146022; MUID:93091248
A;Accession: 146022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Reference number: S26596
A; Accession: S26596
A; Status: preliminary
A; Molecule type: mRNA
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A;Description: Sequence and pattern of expression of a bovine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Graves disease mitochondrial solute carrier protein -
C;Species: Bos primigenius taurus (cattle)
C;Date: 20-reb-1995 #sequence_revision 20-reb-1995 #tc
C;Accession: $26596; I46022
                               R; Lin,
                                                        C; Accession: D84798
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A; Residues: 1-330 <FI2>
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A;Residues: 1-330 <FIE>
A;Cross-references: EMBL:X66035; NID:g386; PIDN:CAA46834.1;
A:Cross-references: EMBL:X66035; NID:g386; PIDN:CAA685; NID:g386; PIDN:CAA685; NID:g386; PIDN:CAA685; NID:g386; PIDN:CAA685; NID:g386; PID
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  Н.;
                                                                                                                                                                                                                                                                                                                             L-EGSPQLNMVGLFRRIISKEGI-PGLYRGITPNFMKVLPAVGISYVVYENMKQ 470
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TRLAVGKTGQ--YSGIYDCAKKILKHEG--LGAFYKGYVPNLLGIIPYAGIDLAVYELLK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WWRQLLAGGIAGAVSRTSTAPLDRLKIMMQVHGSKSDKMNIFGGFRQMVKEGGIRSLWRG
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                                 Kaul, S.;
     Moffat,
Rounsley, S.D.; Shea, K.S.; Cronin, L.A.; S)
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Pred. No. 2.1e
54; Mismatches
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Shen, M.;
                               T.P.;
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  VanAken, S.E.;
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Umayam, L.;
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                         C.Y.;
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                         SLTIPDEFTEDEKKSGOWWRQ-
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A; Experimental sour C; Genetics: C; Genetics: A; Map position: 5 A; Introns: 144/3; 1 A; Note: F7A7.20
                                                                                                                                                                                                                                                                                               hypothetical protein F7A7.20 - Arabidopsis thaliana (;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 C;Accession: T48171 R;Bevan, M.; Terryn, N.; Ardiles, W.; Buysshaert, C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Gene: At2g37890
A;Map position: 2
C;Superfamily: ADP,ATP carrier
C;Keywords: mitochondrion
                                                                                                                                                                                                                                                                ewes, H.W.; Rudd, S.; Len
submitted to the Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-348 <ST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Title: Sequence and analysis of chromosome A; Reference number: A84420; MUID:20083487 A; Accession: D84798
                                                                                                                                                                 A; Cross-references:
                                                                                                                                                                                   A; Molecule type: DNA A; Residues: 1-415 <BEV>
                                                                                                                                                                                                                A; Status: preliminary
                                                                                                                                                                                                                                 A; Reference number: A; Accession: T48171
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C;Genetics:
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Best Local S
Matches 107
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Best Local
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 cal Similarity
107; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   FMTYDALRRLL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LVRTRMQAQAMLEGSP-----QLNMVGLFRRIISKEGIPGLYRGITPNFMKVLPAVGIS
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   Conservative
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                                                                                                                                                                                                                                                               S.; Lemcke, K.;
Protein Sequence
                                                                                                  163/3;
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ce: cultivar Columbia;
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               18.4%;
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                                                                                                                                                                                                                                                                  Mayer, K.I
Database,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 475; DB 2;
Pred. No. 5.2e-24;
2; Mismatches 103
             Score 455.5;
Pred. No. 1.3
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   Mismatches
                                                                                                  231/3;
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                                                                                                                                                                                                                                                                                   K.F.X.
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             1.3e-22;
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                                                                                                  254/3; 292/2;
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 115;
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                                                                                                                                                                                                                                                                                                   R.;
Gaps
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-LLAGGIAGAVSRTSTAPLDRLKIMM 222

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hypothetical protein F20B18.290 - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein [imported] - Arabidopsis thaliana
C; Species: Arabidopsis thaliana (mouse-ear cress)
C; Species: Arabidopsis thaliana (mouse-ear cress)
C; Date: 28-Jul-2000 #sequence_revision 28-Jul-2000 #text_change 28-Jul-2000
C; Accession: T51158
R; Comella, P.; Wu, H.J.; Laudie, M.; Berger, C.; Cooke, R.; Delseny, M.; Grellet, F.
Plant Mol. Biol. 41, 687-700, 1999
A; Title: Fine sequence analysis of 60 kb around the Arabidopsis thaliana AtEml locus
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A; Introns: 116/3;
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C;Genetics:
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A; Accession: T51158
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                                                                                                                                                                                                    PEEYRKKAQSSLTTAVLSAGIATLTC----YPLDTVRRQMQ----MRGTPYKSIPEAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGGIAGAVSRTSTAPLDRLKIMMQVH----GSKSDKMNIFGGFRQMV----KEGGIRSLW
                                                                                                                                                                                                                                        WLDNFAKDSVNPGVMVLLGCGALSSTCGQLASYPLALVRTRMQAQAMLEGSPQLNMVGLF
                                                                                                                                                                                                                                                                                                                                                                                RGNGTNVIKIAPETAVKFWAYEQYKKLLTEEGQKIGTFERFISGSMAGATAQTFIYPMEV 311
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                                                                                                                               AGIIDRDGLIGLYRGFLPNALKTLPNSSIRLTTFDMVKRLIATSEK
                                                                                                                                                                RRIISKEGIPGLYRGITPNFMKVLPAVGISYVVYENMKQTLGVTQK
                                                                                                                                                                                                                                                                           LRLRLAV--EPRYRTMSQVALSMLRDEGIASFYYGLGPSLVGIAPYIAVNFCIFDLVKKS
                                                                                                                                                                                                                                                                                                         MKTRLAVGKTGQYSGIYDCAKKILKHEGLGAFYKGYVPNLLGIIPYAGIDLAVYELLKSY 371
                                                                                                                                                                                                                                                                                                                                                                                                                  AGALAGAAAKTYTAPLDRIKLLMQTHGIRLGQQSAKKAI--GFIEAITLIAKEEGVKGYW
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                                                                                                                                                                                                                                                                                                                                              KGNLPQVIRVLPYSAVQLLAYESYKNLFKGKDDQLSVIGRLAAGACAGMTSTLLTYPLDV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YKKLFRGKDGQLSVLGRLGAGACAGMTSTLITYPLDVLRLAV-EPG-YRTMSQVALNM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QTHGVRAGQQSAKKAI--GFIEAITLIGKEEGIKGYWKGNLPQVIRIVPYSAVQLFAYET
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             l Similarity
98; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     135/3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   156/3; 175/3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 454.5;
Pred. No. 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches 104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   203/3; 226/3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1.3e-22;
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8
                                                                                                                          A; Map position: 4
A; Introns: 181/3;
A; Note: F8B4.100
                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-392 <BEV>
A; Cross-references: EMB
                                                                                                                                                                                                                                                                                                                                  C;Accession: T05350
R;Bevan, M.; Terryn, N.; Ardiles, W.; Buysshaert,
                                                                                                                                                                                                                                                                                                                                                                           adenylate translocator brittle-1 homolog F8B4.100 - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 23-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT
T05350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            В
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A;Note: F20B18.290
C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Map position: 4
A: Tritrons: 46/3; 75/2; 144/3; 181/1; 242/3; 284/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Experimental source: cultivar Columbia; BAC clone C; Genetics:
                                                                                                                                                                                                                                                                       A; Reference number: A; Accession: T05350
                                                                                                                                                                                                                                                                                                      ewes, H.W.; Mayer, K.F.X.; Schuel submitted to the Protein Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-325 <BEV>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Reference number: Z15263
A; Accession: T04273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Bevan, M.; Rose, M.; Hempel, S.; Entian, K.D.; Hoheisel, J.; Mewes, submitted to the Protein Sequence Database, March 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Accession: R; Bevan, M.;
                                                                                                                                                                                  C; Genetics:
                                                                                                                                                                                                  A; Experimental source:
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Matches 124
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                                      Local Sin
hes 124;
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   GIPLGQDAEEKIFTTGDVNKDGKLDFEEFMK----YLKDHEKKMKLAFKSLDKNNDGKIE 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YVVYENMKQTLGV 474
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SGSMAGATAQTFIYPMEVMKTRLAVGKTGQ-----YSGIYDCAKKILKHEGLGAFYK 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EGEEKNGIIDSIPLFAKELIAGGVTGGIAKTAVAPLERIKILFQTRRDEFKRIGLVGSIN
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                                     Similarity 28.8
24; Conservative
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31.9%;
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Pred. No. 2.9e-22;
71; Mismatches 108
                                     Score 446; DB 2
Pred. No. 5e-22;
7; Mismatches 1
                                                                                                                                                                                                                                                                                                        Database,
                                                                                                                                                                                                                                                                                                        February 1999
                                                                                                                                                                                                  clone
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                                      10;
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ОУ	Оy	Qу Оъ	Qу	Qy Db	Qy Db	ОУ
463 376	403 316	345 260	285 201	228 144	168 96	108 65
463 VVYENMKQTL 472 : : 376 MCYEACKKIL 385	SYPLALVRTRMQAQAMLEGSPQLNMVGLERRIISKEGIPGLYRGITPNEMKVLPAVGISY 462 :: : :	KGYVPNLLGIIPYAGIDLAVYELLKSYWLDNFAKDSVNPGVMVLLGCGALSSTCGQLA 402 	KIGTFERFISGSMAGATAQTFIYPMEVMKTRLAVGKTGQYSGIYDCAKKILKHEGLGAFY 344 	228 KSDKMNIFGGFROMVKEGGIRSLWRGNGTNVIKIAPETAVKFWAYEQY-KKLLTEEGQ 284 : :	HSTGIDIGDSLTIPDEFTEDEKKSGQWWRQLLAGGIAGAVSRTSTAPLDRLKIMMQVHGS 227 	ASEIVQSIQTLGLTISEQQAELILQSIDVDGTMTVDWNEWRDYFLFNPVTDIEEIIRFWK 167
	462 375	02 15	44 59	84 00	27 43	6 7

Search completed: August 18, 2002, 09:23:25 Job time: 3574 sec

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Minimum
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Maximum Match
Listing first
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     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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ALIGNMENTS

STANDARD;

PRT;

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EMBL: 272511; CAA96658.1; -.
WOTMPED: F55A11.4; CEO5946.
InterPro; IPR002048; EF-hand.
InterPro; IPR002067; Mtt_carrier.
InterPro; IPR002067; Mttoch_carrier.
InterPro; IPR00193; Mitoch_carrier.
InterPro; IPR00193; Mitoch_carrier.
Pfam; PF00153; mito_carr; 3.
Pfam; PF00153; mito_carr; 3.
PFINTS; PR00926; MITOCARRIER.
SMART; SM00054; EFh; 3.
PROSITE; PS00018; EF_HAND; 2.
PROSITE; PS00215; MITOCH_CARRIER; FALSE_NEG.
Hypothetical protein; Mitochondrion; Inner mem
Transmembrane: T
TRANSMEM 252
TRANSMEM 307
TRANSMEM 452
TRANSMEM 403
TRANSMEM 446
TRANSMEM 504
CA_BIND 52
CA_BIND 52
CA_BIND 86
DOMAIN 123
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-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL INNER MEMBRANE (BY SIMILARITY).

-!- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY. ARALA!
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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STRAIN-BRISTOL N2;
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001 (Rel. 40, Last annotation carrier F55All.4.
Calcium-binding.

(POTENTIAL).

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                                                                             Submitted (AUG-1995) to the EMBL/GenBank/DDBJ-!- FUNCTION: CALCIUM-DEPENDENT MITOCHONDRIAL
                                                                                                       STRAIN=BRISTOL N2;
                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                          Eukaryota; Metazoa; Nemat
Rhabditidae; Peloderinae;
 between
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                                                                                                McMurray A.A.;
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                                                    SIMILARITY).
SUBCELLULAR LOCATION: INTEGRAL MEMBRANE INNER MEMBRANE (BY SIMILARITY).
                                   SIMILARITY: BELONGS SUBFAMILY.
                         SIMILARITY: CONTAINS 4 EF-HAND CALCIUM-BINDING DOMAINS
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InterPro; IPR002048; EF-hand.
InterPro; IPR002067; Mit_carrier
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                                                         CFYKGYLPNLLGIIPYAGIDLTVYESLKSMY-TKYYTEHTEPGVLALLACGTCSSTCGQL
                                                                                                                                                                                                                                                                                                                       TMTVDWNEWRDYFLFNPVTDIEEIIRFWKHSTG-----
: :|: ||::|: | | ||:::: ||:|:
ASYPLALVRTRLQARAI - - -
            ASYPLALVRTRMQAQAMLEGSPQLN-----MVGLFRRIISKEGIPGLYRGITPNFMK
                                                                         AFYKGYVPNLLGIIPYAGIDLAVYELLKSYWLDNFAKDSVNPGVMVLLGCGALSSTCGQL
                                                                                                                     GAELSTIERLLAGSSAGAISQTAIYPMEVMKTRLALRRTGQLDKGMFHFAHKMYTKEGIK 428
                                                                                                                                   DEFTEDEKKSGQWWRQLLAGGIAGAVSRTSTAPLDRLKI---
                                                                                                                                                                                                                                                                                                       SSSYNLNEFQDFMLLYPSTDMRDMYDFWRHNLYCTCLESNSRFRTQNFQIIDIGEDGQVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                           EQPTRYETLFQALDRNGDGVVDIGELQEGLRNLGIPLGQDAEEKIFTTGDVNKDGKLDFE 78
                                                                                                                                                                                NSTKTNKLGVVSCVHLLHAEGGIKSFWRGNGINVIKIAPESAMKFMCYDQIKRWMQEYKG
                                                                                                                                                                                                                                           EDFTPQELLSGVWWRHLVAGGVAGAMSRTCTAPFDRIKVYLQVMYLHLLFHIMFLKALQV
                                                                                                                                                                                                                                                                                                                                                                  DFTNYVIAHEARLAEVFDKIDLNSDGEVDMAEIKSYCKEMGVNLDDQKAMSIVKKMDQSG
                                                                                                                                                                                                                                                                                                                                                                                             EFMKYLKDHEKKMKLAFKSLDKNNDGKIEASEIVQSLQTLGLTISEQQAELILQSIDVDG 138
                                                                                                                                                                                                                                                                                                                                                                                                                              EKEKKIRDMYDRLDADNDGSIDIRDLTQAL-SLQAHIPASVAPKLLERMKSEHSDRVTYA 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
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PS00215; MITOCH_CARRIER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                265
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Transport;
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1 (POTENTIAL).
2 (POTENTIAL).
3 (POTENTIAL).
4 (POTENTIAL).
5 (POTENTIAL).
6 (POTENTIAL).
SPKNSTQPDTMVGQFKHILQTEGFTGLYRGITPNFMK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Score 988.5; DI
; Pred. No. 5e-57;
91; Mismatches 1
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EF-HAND 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ANCESTRAL CALCIUM SITE 3. EF-HAND 4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                membrane; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         137;
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                                                                                                                                                                                                                                                                          VQMM--
541
                          453
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15;

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RESULT
CMC1_Y
Transmembrane;
TRANSMEM 231
TRANSMEM 307
TRANSMEM 355
TRANSMEM 409
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                                                                                                   Pfam; PF00036; efhand; 3. Pfam; PF00153; mito_carr; 3. PRINTS; PR00926; MITOCARRIER.
                                                                                                                                                                             SGD;
                                                                                                                                                                                         EMBL;
                                                                                                                                                                                                                            modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                            PROSITE; PS00018; EF_HAND; 1.
PROSITE; PS00215; MITOCH_CARRIER; 1.
Hypothetical protein; Mitochondrion; Inner
                                                                                                                                                                                                                                                                                                         This
                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-97321806; PubMed-9178508;
el Moualij B., Duyckaerts C., Lamotte-Brasseur J.,
"Phylogenatic classification of the mitochondrial of
Saccharomyces cerevisiae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-OCT-2001 (Rel. 40, La: 16-OCT-2001 (Rel. 40, La: Probable calcium-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YEAST
                                                                                                                                                                                                      EMBL;
                                                                                                                                                                                                                                                                             the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                           -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of six ORFs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Poehlmann R., Philippsen P.; "Sequencing a cosmid clone of Saccharomyces cerevisiae chromosome reveals 12 new open reading frames (ORFs) and an ancient duplication."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Soler-Mira A., Saiz J.E., Ballesta J.P.G., Remacha M. "The sequence of a 17,933 bp segment of Saccharomyces chromosome XIV contains the RHO2, TOP2, MKT1 and END3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=S288C / FY1679;
MEDLINE=96310628; PubMed=8740422;
                                                                                                                                        InterPro;
                                                                                                                                                   InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Yeast 13:573-581(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 new open reading frames
Yeast 12:485-491(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Saccharomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Saccharomyces cerevisiae (Baker's yeast).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    reast 12:391-402(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=S288C / FY1679;
WEDLINE=96267764; PubMed=8701611;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6-OCT-2001
                                                                                                                                                                                                                                                                                                                                            SIMILARITY: CONTAINS 4 EF-HAND CAUTION: REF.1 AND REF.2 SEQUEN
                                                                                                                                                                                                                                                                                                                                                                              inner membrane (Potential).
SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER
                                                                                                                                                                                                                                                                                                                                                                                                          SUBCELLULAR LOCATION: Integral membrane
                                                                                                                                                                                                                                                                                                                                CAUTION: REF.1 AND REF.2 SE FRAMESHIFT IN POSITION 403.
                                                                                                                                                                                                                                                                                                                                                                                                                                  FUNCTION: CALCIUM-DEPENDENT MITOCHONDRIAL
                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY)
                                                                                                                                                                             ; Z71359; CAA95958.1; S0005027; YNL083W.
                                                                                                                                                                                                                                                                                         SWISS-PROT entry is copyright. It is produced through sen the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                     x89016;
                                                                                                                                                                                                                                                                   non-profit institutions as long
                                                                                                                                    IPR002048; EF-hand.
IPR002067; Mit_carrier.
IPR001993; Mitoch_carrier.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fungi;
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307
355
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           ; Transport;
31 248
07 326
55 368
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                frames.";
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                                                 Calcium-binding.
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(POTENTIAL).
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Best Local S
Matches 155
                                                                                          Grave's disease carrier protein homolog). SLC25A16 OR GDA OR GDC.
                                                                                                                                                     GDC_BOVIN STANDARD; PRT; GDC_BOVIN STANDARD; PRT; GO1188; 01-APR-1993 (Rel. 25, Created) 01-APR-1993 (Rel. 25, Last sequence up 01-MAR-2002 (Rel. 41, Last annotation
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                                                                         Bos taurus (Bovine).
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Pred. No. 1.3e-32;
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6 (POTENTIAL).
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EF-HAND 2.
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(GDC) (Mitochondrial solute carrier
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Mammalia; Bovidae; E

Bovinae;

Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Cetartioda

Cetartiodactyla;

Ruminantia;

Craniata;

Vertebrata; Euteleostomi;

Pecora;

Bovoidea;

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SEQUENCE FROM
TISSUE=Heart;
P16260;
01-AUG-1990 (Rel.
01-JUL-1993 (Rel.
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REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; X66035; CAA46834.1; -. PIR; S26596; S26596.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Sequence and pattern of expression of a bovine mitochondrial transport protein associated with DNA Seq. 3:71-78(1992).
                                                     GDC_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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InterPro; IPR001993; Mitoch_carrier.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FUNCTION: Required for the accumulation mitochondrial matrix (By similarity). SUBCELLULAR LOCATION: Integral membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                inner membrane (By similarity).
TISSUE SPECIFICITY: MOSTLY IN THYROID,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                        NGTNVIKIAPETAVKFWAYEQYKKLLTEEGQKIGTFERFISGSMAGATAQTFIYPMEVMK 313
                                                                                                                                         LPEFEKCLTMRETMKYVYGHHGIRKGLYRGLSLNYIRCVPSQAVAFTTYELMKQ
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                                                                                                                                                                                                                                                                          VRLAFQVKGEHTYTGIIHAFKTIYAKEGGFLG-FYRGLMPTILGMAPYAGVSFFTFGTLK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             112;
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Pred. No. 2.3e
54; Mismatches
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POTENTIAL
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bovine homologue of a human
d with Grave's disease.";
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MEDLINE-93091248; PubMed-1457817; Fiermonte G., Runswick M.J., Walk "Sequence and pattern of expressimitochondrial transport protein a
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or send an
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Zarrilli R., Oates E.L., McBride O.W., Lerman M.I., Chan J.Y.,

Santisteban P., Ursini M.V., Notkins A.L., Kohn L.D.;

"Sequence and chromosomal assignment of a novel cDNA identified immunoscreening of a thyroid expression library: similarity to a family of mitochondrial solute carrier proteins.";

family of mitochondrial solute carrier proteins.";

Mol. Endocrinol. 3:1498-1508(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Grave's disease carrier (GDA) (Mitochondrial so: SLC25A16 OR GDA.
                                                                                                                                                Mitochondrion;
                                                                                                                                                                                                          Pfam; PF00153; mito_carr;
                                                                                                                                                                                                                                                                        MIM; 139080;
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                                                                                                                                                                                                                                                                                                                                                                                               modified
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Prohl C., Pelzer W.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human)
                                                                                                                                                                                      PRINTS; PR00926; MITOCARRI
                                                                                                                                                                                                                               InterPro; IPR002067; Mit_carrier.
InterPro; IPR001993; Mitoch_carrier.
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REVISIONS TO C-TERMINUS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The yeast mitochondrial carrier Leu5p and
                                                                                                                                                                                                                                                                                                                                                 s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the Ew European Bioinformatics Institute. There are no restr by non-profit institutions as long as its content ified and this statement is not removed. Usage by and its requires a license agreement (See http://www.isb-send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DISEASE: POSSIBLE ROLE IN GRAVES' DISEASE. THIS PROTEIN RECOGNIZED BY IGG FROM PATIENTS WITH ACTUE GRAVE'S DISISINLARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY CAUTION: REF.1 SEQUENCE DIFFERS FROM THAT SHOWN FROM POSONWARD DUE TO A FRAMESHIFT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
DISEASE: POSSIBLE ROLE IN GRAVES' DISEASE. THIS PROTEIN IS
RECOGNIZED BY IGG FROM PATIENTS WITH ACTIVE GRAVE'S DISEASE.
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                                                                                                                                                                     MITOCH_CARRIER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PubMed=11158296;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           matrix.
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211
254
123
219
                                                                                 r membrane; Repeat; T
154 POTENTIAL.
211 POTENTIAL.
254 POTENTIAL.
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solute carrier
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    CFDB8F4F3E7F0F4B
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                                                                                                                                                                                                                                                                                                                                                                         http://www.isb-sib.ch/announce/
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    CRC64;
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Similarity

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Score Pred.

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DB 1; e-22;

Length 332;

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SO THE TWO RESERVED TO THE RES
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=90114217; PubMed=2575220;
Zarrilli R., Oates E.L., McBride O.W., Lerman M.I., Chan J.Y.,
Santisteban P., Ursini M.V., Notkins A.L., Kohn L.D.;
"Sequence and chromosomal assignment of a novel cDNA identifie immunoscreening of a thyroid expression library; similarity to family of mitochondrial solute carrier proteins.";
Mol. Endocrinol. 3:1498-1508(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence up
01-MAR-2002 (Rel. 41, Last annotation
Grave'S disease carrier protein (GDC)
protein homolog) (Fragment).
SLC25A16 OR GDA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                  Mitochondrion;
                                                                                                                                                                                                            PROSITE;
                                                                                                                                                                                                                                                                                    EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- DOMAIN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Thyroid
                                                                                                                                      REPEAT
                                                                                                                                                                                                                                                          InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              371
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial inner membrane (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YWLDNF----AKDSVNPGVMVL----LGCGALSSTCGQLASYPLALVRTRMQAQAML-
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                                                                                                                                                                                               PF00153; mito_carr; 3. TE; PS00215; MITOCH_CARRIER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EFEKCLTMRDTMKYDYGHHGIRKGLYRGLSLNYIRCIPSQAVAFTTYELMKQ
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                                                                                                                                                                                                                                                                                    М32973;
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                                                                                                                                                                                                                                                        IPR001993; Mitoch_carrier.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPOSED OF THREE HOMOLOGOUS DOMAINS
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223
322
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3 322
3 35056 MW; 35056 MW;
                                                                                                                                                                                                                                                                                  AAA41639.1;
                                                                                                                                                                                  Transmembrane;
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                                                                                                                                                                               Transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Craniata; Vertebrata; I
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                        F78CBDA36CA9DC9A CRC64;
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(Mitochondrial solute carrier
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Murinae; Rattus.
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                                                                      Pfam; pF0013; mito_carr; 3.

Pfam; pF0013; mito_carrier.

PRINTS; pR00926; MITOCH_CARRIER; 1.

PROSITE; PS00215; MITOCH_CARRIER; 1.
                                                                                                                                                                                                                                        use by non-profit institumodified and this statement entities requires a license
                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content
                                                                                                                                                                                            EMBL; M79333;
                                                                                                                                                                                                                            or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                 -i- SUBCELLULAR LOCATION: Chloroplast; amyloplast.
-i- TISSUE SPECIFICITY: ENDOSPERM OF DEVELOPING KERNELS.
-i- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                     Suppressor-mutator-induced m Plant Cell 3:1337-1348(1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sullivan T.D., Strelow Nelson O.E. Jr.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-APR-1993 (Rel.
01-APR-1993 (Rel.
16-OCT-2001 (Rel.
                                                                                                                                                           MaizeDB; 47578;
                                                                                                                                                                             PIR; JQ1459; JQ1459.
                                                                                                                                                                                                                                                                                                                                                                                                                                    "Analysis of maize brittle-1 alleles and a Suppressor-mutator-induced mutable allele.
                                                                                                                           InterPro; IPR002067; Mit_carrier.
InterPro; IPR001993; Mitoch_carrier.
                                                                                                                                                                                                                                                                                                                                                                                                    -!- FUNCTION: COULD PLAY A ROLE IN AMYLOPLAST MEMBRANE TRANSPORT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=93005685; PubMed=1668652;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=4577;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Zea mays (Maize)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      103;
 peptide; Chloroplast; Amyloplast; Transmembrane.

1 75 CHLOROPLAST (POTENTIAL).

76 436 BRITTLE-1 PROTEIN.

M 229 247 POTENTIAL.

M 327 347 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
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25, Last sequence updat
40, Last annotation upd
, chloroplast precursor.
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35.6%;
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Last annotation update)
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                                                                                                                                                                                                                       is not removed. Usage by and to include is not removed. Usage by and to include is arreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 428;
Pred. No. 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Illingworth C.A., Phillips R.L.,
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                 013805;
15-JUL-1998
15-JUL-1998
                                                             InterPro; IPR002067; Mit_carrier.
InterPro; IPR001993; Mitoch_carrier.
Pfam; PF00153; mito_carr; 3.
                                                                                                                           modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Ew the European Bioinformatics Institute. There are no restructed by non-profit institutions as long as its content
                                                                                                                                                                                                                                                                         Skelton J., Churcher C.M., Barrell B.G., Rajandream M.A., Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: Integral membrane protein. Mitoo
                                                                                                                                                                                                                                                                                                                                                                                            Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                       Putative mitochondrial carrier C17H9.08. SPAC17H9.08.
                                                                                                  EMBL; 298597; CAB11217.1;
                                                                                                                                                                                                                                                                                                                 STRAIN=972;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SCHPO
 TRANSMEM
            Transmembrane;
                        Hypothetical protein; Mitochondrion;
                                    PRINTS; PR00926; MITOCARRIER, PROSITE; PS00215; MITOCH_CARRIER;
                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=4896;
                                                                                                                                                                                                                                                                                                                                                                      Schizosaccharomyces.
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                                                                                                                                                                                                                                                               inner membrane (Potential)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGFASTLCTYPMELIKTRVTIEK-DVYDNVAHAFVKILRDEGPSELYRGLTPSLIGVVPY
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36, Last sequence update)
36, Last annotation updat
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                                                                                                                                                                                           EMBL outstation
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Best Local S
Matches 94
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P32007;
01-JUL-1993 (Rel. 26, Creater,
01-JUL-1993 (Rel. 26, Last sequence update,
16-OCT-2001 (Rel. 40, Last annotation update)
TO ATP carrier protein, isoform T2 (ADP/ATP
  entities
or send a
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SEQUENCE
                                                                                                  the
                                                                                                                                                                                                                                                                                                                                       "Two bovine genes for mitochondrial ADP/ATP translocase differences in various tissues.";
Biochemistry 28.866-873(1989).
-!- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACRO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           190 KSGQWWRQLLAGGIAGAVSRTSTAPLDRLKIMMQVH-----GSKSDKMNIFGGFRQMVKE 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                73
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European Bioinformatics Institute. There are no rest by non-profit institutions as long as its content ified and this statement is not removed. Usage by artities requires a license agreement (See http://www.isb-send an email to license@isb-sib.ch).
                                                                                                                                                                                            SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
                                                                                                                                                                                                                        DOMAIN: COMPOSED OF
                                                                                                                                                                                                                                                                   SUBCELLULAR LOCATION: Integral membrane protein.
                                                                                                                                                                                                                                                                                            SUBUNIT: HOMODIMER.
                                                                                                                                                                                                                                                                                                                   MITOCHONDRIAL INNER MEMBRANE
                                                                                                                                                                                                                                               inner membrane
                                                                                                                      SWISS-PROT entry is copyright. It is produced through a sen the Swiss Institute of Bioinformatics and the EMBI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGIRSLWRGNGTNVIKIAPETAVKFWAYEQYKKLLTEEGQKIGTFERFISGSMAGATAQT 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BOVIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VTLTGIFPYAGMSFLAYDLA----TDFFHKQKIDEWVSTKKSDKKLKTWPELLCGAFAGV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KSG-----IAGGTAGCVAKSVVAPLDRVKILYQTNHASYRGYAYSRHGLYKAIKHIYHV 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VSTSFFVYNHSKALLGI
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326
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PubMed=2540808;
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211
260
314
37059
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29.7%;
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                                                                                                                                                                                                                        THREE HOMOLOGOUS DOMAINS
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Pred. No. 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   298
                           (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1;
.2e-18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            translocase 3) (Adenine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CRC64
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                                                                                             restrictions
                                                    and for
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                                                                                                                           EMBL outstation
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                                                                                                                                                                                                                                                                                                                                            THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             42;
                                                                                                                                             collaboration
                                                                           H
                                                  ons on its in no way commercial
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Matches 96
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                                                                                                                                                          ADT3_HUMAN STANDARD; PRT; 298 AA.
P1235; Q96C49;
O1-CCT-1989 (Rel. 12, Created)
O1-NOV-1990 (Rel. 16, Last sequence update)
O1-MAR-2002 (Rel. 41, Last annotation update)
ADP,ATP carrier protein, liver isoform T2 (ADP/ATP translocase (Adenine nucleotide translocator 3) (ANT 3).
SLC25A6 OR ANT3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TRANSMEM
TRANSMEM
                                                                                                                     Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
NCBI_TaxID=9606;
                                                                                                                                                                                                                                            NAMDH
 Submitted (OCT-2001) to
                   SEQUENCE FROM N.A.
TISSUE=Cervix;
                                                            ADP/ATP
                                                                                        SEQUENCE FROM N.A. MEDLINE=89236396; PubMed=2541251;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PR00926; MITOCARRIER; PROSITE; PS00215; MITOCH_CARRIER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIR;
           Strausberg
                                                             "DNA sequences of two expressed AND/ATP translocase.";
                                                                               Cozens A.L., Runswick M.J.,
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                                                   Mol. Biol.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            В43646; В43646.
                                                                                                                                                                                                                                                                                  KGADIMYKGTVDCWRKILKDEGGKAFFKGAWSN---VLRGMGGAFVLVLYDELKKVI
                                                                                                                                                                                                                                                                                                                        AYFGIYDTAK-----GMLPDPKNTHIVVSWMIAQTVTAVAGVVSYPFDTVRRRMMMQSGR
                                                                                                                                                                                                                                                                                                                                          IDLAVYELLKSYWLDNFAKDSVNPGVMVLLGCGALSSTCGQLASYPLALVRTRMQAQAML
                                                                                                                                                                                                                                                                                                                                                               FVYPLDFARTRLAADVGKSGSEREFRGLGDCLVKITKSDGIRGLYQGFNVSVQGIIIYRA
                                                                                                                                                                                                                                                                                                                                                                                   FIYPMEVMKTRLA--VGKTG---QYSGIYDCAKKILKHEGLGAFYKGYVPNLLGIIPYAG
                                                                                                                                                                                                                                                                                                                                                                                                       FWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKRTQFWRYFAGNLASGGAAGATSLC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                            translocase.
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IPR001993; Mitoch_carrier.
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73
117
176
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                                                   206:261-280(1989)
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EMBL/GenBank/DDBJ databases
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Pred.
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                                                                                                                              Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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                                                                     human
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                                                                     mitochondrial
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CONFLICT
CONFLICT
SEQUENCE
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SEQUENCE OF 3
TISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                  TRANSMEM
REPEAT
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PIR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Two distinct genes for ADP/ATP translocase are level in adult human liver.";
Proc. Natl. Acad. Sci. U.S.A. 85:377-381(1988).
-!- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND MITOCHONDRIAL INNER MEMBRANE.
-!- SUBUNIT: HOMODIMER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            entities requires a license agreement (Some send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                        REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                       TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                 Multigene
                                                                                                                                                                                                                                                                                                                                                                                                                           Mitochondrion; Inner
                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00215; MITOCH_CARRIER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MIM; 403000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=88124845;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro;
           420
                                  190
                                                        360
                                                                              130
                                                                                                     305
                                                                                                                                                250
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBCELLULAR LOCATION:
                                                                                                                                                                                S03894; S03894.
B28116; B28116.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           inner membrane
AYFGVYDTAK-----GMLPDPKNTHIVVSWMIAQTVTAVAGVVSYPFDTVRRRMMMQSGR
                                                                                          FIYPMEVMKTRLA--VGKTG---QYSGIYDCAKKILKHEGLGAFYKGYVPNLLGIIPYAG
                                                                                                                         FWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLASGGAAGATSLC
                                                                                                                                                LWRGNGTNVIKIAPETAVKFWAYEQYKKLLTEEGQKIGTFERFISGSM-----AGATAQT
                                                                                                                                                                   FVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVSVQGIIIYRA
                                                     IDLAVYELLKSYWLDNFAKDSVNPGVMVLLGCGALSSTCGQLASYPLALVRTRMQAQAML
                                                                                                                                                                                                                                                                                                                                                                                                                                                Pro; IPR002067; Mit_carr
Pro; IPR001993; Mitoch_c
Pr00153; Mito_carr; 3.
S; PR00926; MITOCARRIER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          J03592; AAA36750.1; - BC014775; AAH14775.1;
                                                                                                                                                                                                                   97;
                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       36-298 FROM
                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Attardi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PubMed=2829183;
                                                                                                                                                                                                                                                                          242
32866
                                                                                                                                                                                                                                                                                                  29
91
134
195
231
231
200
100
208
298
                                                                                                                                                                                                                            14.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mit_carrier.
Mitoch_carrier.
                                                                                                                                                                                                                                                                                                                                                                                                                           membrane;
                                                                                                                                                                                                                                                                           Œ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Integral
                                                                                                                                                                                                                                                              3.

KHTQ -> RHA (IN REF. 3

KHTQ -> F (IN REF. 2).

S -> F (IN REF. 2).

MW; 18534E9F0E49672F CR
                                                                                                                                                                                                                   60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    THE MITOCHONDRIAL CARRIER FAMILY
                                                                                                                                                                                                                            Score 368; DB 1;
Pred. No. 4e-17;
                                                                                                                                                                                                                                                                                                                                          (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                          Repeat;
                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                           Transmembrane; Transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAINS
                                                                                                                                                                                                                   112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein.
                                                                                                                                                                                                                                       Length
                                                                                                                                                                                                                                                                           CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         at the mRNA
                                                                                                                                                                                                                   28;
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                                                                                                                                                                                                                  Gaps
                                                                              189
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                                                                                                                                                304
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밁

245

KGADIMYTGTVDCWRKIFRDEGGKAFFKGAWSN---VLRGMGGAFVLVLYDELKKVI 298

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Query Match
Best Local
         Matches
                                                       TRANSMEM
TRANSMEM
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SEQUENCE
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P38702;
                                                                                                                                                                                                                                                                                                                       Mo1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Dover J., Du Z., Favello A., Fulton L., Gattung S., Geisel C., Kirsten J., Kucaba T., Hillier L., Jier M., Johnston L., Langston Y., Kucaba T., Hillier L., Jier M., Johnston L., Langston Y., Macri C., Mardis E., Menezes S., Mouser L., Nhan M., Rifkin L., Riles L., St Peter H., Trevaskis E., Vaughan K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YEAST
                                                                                                                                SGD; S0001044; LEU5.
InterPro; IPR002067; Mit_carrier.
InterPro; IPR001993; Mitoch_carrier
                                                                                                                                                                                                                         use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Saccharomyces cere
Eukaryota; Fungi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LEU5
                                                                                                                          Pfam; PF00153; mito_carr;
                                                                                                                                                                                                                                    the
                                                                                                                                                                                                                                                       This
                                                                                                                                                                                                                                                                                                                                                   disease
                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=21106356;
                                                                                                                                                                                                                                                                                                                                                                                                                    Science 265:2077-2082(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=94378003; PubMed=8091229;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mitochondrial carrier
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-FEB-1995
16-OCT-2001
                                                                                               Mitochondrion;
                                                                                                       PROSITE;
                                                                                                                  PRINTS;
                                                                                                                                                                         EMBL; U10555; AAB68424.1;
                                                                                                                                                                                             or send
                                                                                                                                                                                                                                            between
                                                                                                                                                                                                                                                                                                                                          matrix.
                                                                                                                                                                                                                                                                                                                                                           "The yeast mitochondrial carrier
                                                                                                                                                                                                                                                                                                                                                                             Prohl C., Pelzer W.,
                                                                                                                                                                                                                                                                                                                                                                                                   FUNCTION, AND
                                                                                                                                                                                                                                                                                                                                                                                                                                      "Complete nucleotide sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Vaudin M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Vignati D., Wilcox L., Wohldman P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Saccharomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-FEB-1995
                                                                                                                                                                                                                                  European
                                                                                                                                                                                                                                                                      DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS. SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
                                                                                                                                                                                                                                                                                                            mitochondrial matrix.
                                                                                                                                                                                                                                                                                                                       FUNCTION:
                                                                                                                                                                                                                                                                                                  SUBCELLULAR LOCATION: Integral membrane protein.
                                                                                                                                                                                                                                          SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OR YHR002W
                                                                                                                                                                                                                                                                                          inner membrane
                                                                                                                                                                                                                                                                                                                                Cell. Biol.
                                                                                                                                                                 S46795; S46795.
        98;
                                                                                                       pr00926; MITOCARRIER.
; PS00215; MITOCH_CARRIER; 3.
                                                                                                                                                                                             an
                  Similarity
                                                                                                                                                                                                                                                                                                                                                  protein
                                                                                                                                                                                                    pean Bloinformatics Institute. The non-profit institutions as long and this statement is not removed. requires a license agreement (See
                                                      136
208
325
357 /
                                                                                                                                                                                             email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (Rel.
        Conservative
                                                                                                                                                                                                                                                                                                                                                                             SUBCELLULAR LOCATION.
356; PubMed=11158296;
zer W., Diekert K., Kmita
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cerevisiae (Baker's yeast).
ngi; Ascomycota; Saccharomycotina; Saccharomycetes;
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                                                        AA;
                                                                                    Inner membrane; Repeat; 153 POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                 are required
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31,
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                 14.7%;
30.1%;
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        55,
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                 Score 365; DB 1; Pred. No. 7.9e-17;
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                                                        16266B2CD4B996D5
                                                                                                                                                                                                                                                                                                                      accumulation of coenzyme A in
        Mismatches
                                                                                                                                                                                                                                                                                                                                                   accumulation
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                                                                                               Transmembrane;
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                         Length 357;
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         Indels
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        Gaps
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ID ADT2_MOUSE STANDARD
AC P51881; Q61311;
DT 01-CCT-1996 (Rel. 34, C
DT 01-MAR-2002 (Rel. 41, L
DT 01-MAR-2002 (Rel. 41, L
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                                                                                                                 REVISIONS.
Laplace C.
Submitted
                                                                                                                                                                                                              SEQUENCE FROM N.A.
TISSUE-Skeletal muscle;
Sheldon J.G.;
                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                           PubMed=10974536;
Levy S.E., Chen Y.-S.
                                                                                                                                                        Submitted
                                                                                                                                                                 Costet P.,
                                                                                                                                                                         SEQUENCE FROM
STRAIN=129/SV;
                                                                                                                                                                                                                                                       Mamm.
                                                                                                                                                                                                                                                                                  Ellison J.W.,
                                                                                                                                                                                                                                                                                          MEDLINE-97059403;
                                                                                                                                                                                                                                                                                                    STRAIN=C57BL/6; TISSUE=Brain;
                                                                                                                                                                                                                                                                                                              SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                      SLC25A5 OR ANT2
                  ÷
                                                                                               SEQUENCE
                                                                                                                                                                                                                                                            "Rapid evolution omologs.":
                                                                                                                                                                                                      Thesis (1995),
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                  SUBUNIT: HOMODIMER
         SUBCELLULAR LOCATION:
                           MITOCHONDRIAL INNER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IGYIKVTPMVACSFFVYERMKWNFGI
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                                                                                                                                                                                                                                                       Genome
                                                                                               FROM
                                                                                                                                                       (FEB-1993)
                                                                                                                 (FEB-1997)
                                                                                                                                                                                                                                                     7:25-30(1996)
                                                                                                                                                                                   N.A.
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                                                                                                                                                                                                     University
                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                       X., Franc
                                                                                                                                                                                                                                                                                          PubMed=8903724;
                                                                                                                                                                                                                                                                                                                                         Chordata;
Rodentia;
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        Integral
                                    EXCHANGE
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QУ
                                                     "Expression and sequence analysis of translocase 1 and 2 genes."; Gene 254:57-66(2000).
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Last sequence up
Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             pseudoautosomal
                                                                                                                                                                                                EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                 EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                       Cambridge,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Craniata; Ver
Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Shapiro L.J
                                                                                                      Wallace D.C
of the mouse
membrane
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                                                     QF
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thi; Muridae;
                                                     ADP
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                                                      ACROSS
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   Mitochondrial
                                                                                                        nucleotide
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Best Local S
Matches 94
                               ADT2_HUMAN STANDARD; PRT; 298 AA. P05141; 043350; 13-AUG-1987 (Rel. 05, Created) 01-OCT-1994 (Rel. 30, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) ADP, ATP carrier protein, fibroblast isoform (/ Adenine nucleotide translocator 2) (ANT 2).
                                                                                               LT 13
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                          SLC25A5 OR ANT2
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EMBL; U10404; AAA19009.1; --
EMBL; X70847; CAA50196.1; --
EMBL; AF240003; AAF64471.1; --
MGD; MGI:1353496; Slc25a5.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                 REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PR00926; MITOCARRIER, PROSITE; PS00215; MITOCH_CARRIER;
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                                                                                                                                                                                                    FVYPLDFARTKLAADVGKAGAEREFKGLGDCLVKIYKSDGIKGLYQGFNVSVQGIIIYRA
                                                                                                                                                                                                                FIYPMEVMKTRLA--VGKTG---QYSGTYDCAKKILKHEGLGAFYKGYVPNLLGIIPYAG
                                                                                                                                                                                                                                                        LWRGNGTNVIKIAPETAVKFWAYEQYKKLLTEEGQKIGTFERFISGSM----AGATAQT
                                                                                                                                                                                                                                                                                           RQLLAGGIAGAVSRTSTAPLDRLKIMMQV-HGSK---SDKM--NIFGGFRQMVKEGGIRS
                                                                                                                                 KGTDIMYTGTLDCWRKIARDEGSKAFFKGAWSN---VLRGMGGAFVLVLYDEIKK
                                                                                                                                                  EGSPQL--NMVGLFRRIISKEGIPGLYRGITPNFMKVLPAVGISY--VVYENMKQ
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                                                                                                                                                                                                                                        FWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKRTQFWRYFAGNLASGGAAGATSLC
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Pro; IPR001993; Mitoch_carrier.
PF00153; mito_carr; 3.
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Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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Mo. 1.3e-16
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EMBL; M57424; AAA51737.1; -.
EMBL; J02683; AAA35879.1; -.
EMBL; L78810; AAB39266.1; -.
EMBL; AC004000; AAB96347.1; -.
EMBL; J03591; AAA36749.1; -.
EMBL; J03591; AAA36749.1; -.
PIR; C288116; C288116.
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MEDLINE-90375457; PubMed-2168878;
MEDLINE-90375457; PubMed-2168878;
                                                                                                                                                                                                                                                                                                                                                     use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                             Pfam; PF00153; mito_carr; 3.
PRINTS; PR00926; MITOCARRIER.
PROSITE; PS00215; MITOCH_CARRIER;
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InterPro; IPR001993;
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Houldsworth J., Attardi G.;
"Two distinct genes for ADP/ATP translocase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mazzarella
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J. Biol. Chem.
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-1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY
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C. Natl. Acad. Sci. U.S.A. 85:377-381(1988).
FUNCTION: CATALYZES THE EXCHANGE OF ADP AND
MITOCHONDRIAL INNER MEMBRANE.
SUBUNIT: HOMODIMER.
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. Chem. 265:16060-16063(1990)
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la R.A., Schlo
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              the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-FEB-1995 (Rel. 31, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) ADP, ATP carrier protein, fibroblast isoform (
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Q09073;
01-FEB-1995 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                       "Isolation and characterization of cDNA clones and a genomiencoding rat mitochondrial adenine nucleotide translocator. Biochim. Biophys. Acta 1152:192-196(1993).

-i- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS
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Mammalia; Eutheria; Rodentia;
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Shinohara Y., Kamida M., Yamazaki N.,
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SUBCELLULAR LOCATION: Integral membrane
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                                                                                                                                                                                                                                                                                                                                                                MITOCHONDRIAL INNER MEMBRANE.
                                                                                                                                                                                                                                                      SKELETAL MUSCLE.
                                                                                                                                                                                                                                                                                                inner membrane.
                                                                                                                                     SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KGTDIMYTGTLDCWRKIARDEGGKAFFKGAWSN---VLRGMGGAFVLVLYDEIKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EGSPOL--NMVGLFRRIISKEGIPGLYRGITPNFMKVLPAVGISY--VVYENMKQ 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AYFGIYDTAK-----GMLPDPKNTHIVISWMIAQTVTAVAGLTSYPFDTVRRRMMMQSGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IDLAVYELLKSYWLDNFAKDSVNPGVMVLLGCGALSSTCGQLASYPLALVRTRMQAQAML
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKRTQFWRYFAGNLASGGAAGATSLC
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                                                                                                                                                                                                     TO THE MITOCHONDRIAL CARRIER FAMILY.
                                                                                                                                                                                                                               THREE HOMOLOGOUS
                                                                                                                                                                                                                                                                         PRESENT IN KIDNEY,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 359; DB Pred. No. 1.5e S1; Mismatches
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Sciurognathi; Muridae
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5 -> E (IN REF. 2).
7 -> L (IN REF. 4 AN
7 -> G (IN REF. 5).
F973C3AED92C49D3 (
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2) (ANT 2).
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N REF. 4 AND 9
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nes 112;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Muridae;
                                                                                                                                                                                                                                                                                                                   protein.
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Best Local S
Matches 94
                                                                                                                                                                                                                                                                      P25083;
01-MAY-1992
                                                                                                                                                                                                                       01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
ADP,ATP carrier protein, mitochondrial precursor (ADP/ATP translocase)
(Adenine nucleotide translocator) (ANT).
                                            Curr. Genet. 20:405-410(1991).
-!- FUNCTION: CATALYZES THE EXCHANGE
                                                                              STRAIN=CV. DESIREE; TISSUE=Green MEDLINE=9224284; PubMed=1807831; Emmermann M., Braun H.P., Schnitz Emmermann M., Braun H.P., Schnitz "The ADP/ATP translocator from po
                                                                                                                                                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
                                                                                                                                                                                                                                                                                                          SOLTU
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REPEAT
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InterPro; IPR002067; Mit_carrier.
InterPro; IPR001993; Mitoch_carrier.
Pfam; PF00153; mito_carr; 3.
                      -
                                                                  extension.";
                                                                                                                                                                                                   Solanum tuberosum
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                                                                                                                                                    NCBI_TaxID=4113;
                                                                                                                              EQUENCE
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           SUBCELLULAR LOCATION:
                      SUBUNIT: HOMODIMER
                                  MITOCHONDRIAL INNER MEMBRANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FIYPMEVMKTRLA--VGKTG---QYSGIYDCAKKILKHEGLGAFYKGYVPNLLGIIPYAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RQLLAGGIAGAVSRTSTAPLDRLKIMMQV-HGSK---SDKM--NIFGGFRQMVKEGGIRS 249
                                                                                                                                                                                                                                                                                               SOLTU
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                                                                                                                                                                                                                                                                                                                                                                                                       AYFGIYDTAK-----GMLPDPKNTHIFISWMIAQSVTAVAGLTSYPFDTVRRRMMMQSGR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity 31.9
94; Conservative
                                                                                                                              FROM N.A
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                                                                                                                                                                                                                                                                                                STANDARD;
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31.9%;
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                                                                              Schmitz U.K. from potato
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         Integral
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Pred. No. 1.8e-16;
D; Mismatches 113;
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         protein.
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                                                                                amino-terminal
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                                               ACROSS
            Mitochondrial
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Search completed: August 18, 2002, 09:31:11 Job time: 486 sec
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Best Local S
Matches 92
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TRANSIT 1 77 MITOCHE
CHAIN 78 386 ADP,ACH
CHAIN 78 386 ADP,ACH
TRANSMEM 90 107 1 (POTE
TRANSMEM 152 170 2 (POTE
TRANSMEM 155 212 3 (POTE
TRANSMEM 256 275 4 (POTE
TRANSMEM 255 312 5 (POTE
TRANSMEM 255 312 5 (POTE
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PR00926; MITOCARRIER.
PROSITE; PS00215; MITOCH_CARRIER; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00153; mito_carr;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mitochondrion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
                                                                              312 IDTVRRRMMMTSG-EAVKYKSSLDAFSQIVKNEGPKSLFKGAGANILRAVAGAGV 365
                                                                                                                  406
                                                                                                                                               256
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                                                                                                                                                                                                                                                                                                                                                   90
                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 31.2
nes 92% Conservative
                                                                                                                                                                                                                                                                              LALVRTRMQAQAMLEGSPQLNMVGLFRRIISKEGIPGLYRGITPNFMKVLPAVGI 460
                                                                                                                                                                                                                ASGGAAGASSLFFVYSLDYARTRLANDRKASKKGGERQFNGLVDVYKKTLKSDGIAGLYR
                                                                                                                                                                                                                                           ISGSMAGATAQTFIYPMEVMKTRLA----VGKTG---QYSGIYDCAKKILKHEGLGAFYK 345
                                                                                                                                                                                                                                                                                                                                                  EKGFAAFATDFLMGGVSAAVSKTAAAPIERVKLLIQ----NQDEMLKAGRLSEPYKGIGE 135
                                                                                                                                              GFNISCYGIIVYRGLYFGMYDSLKPVLLTGNLQDS----FFASFGLGWLITNGAGLASYP
                                                                                                                                                                             GYVPNLLGIIPYAGIDLAVYELLKSYWLDNFAKDSVNPGVMVLLGCGALSSTCGQLASYP 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       386 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Inner membrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                   14.3%; Score 355.5; DB 1; 31.2%; Pred. No. 3.6e-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     42058 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                   55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADP, ATP CARRIER PROTEIN.

1 (POTENTIAL).

2 (POTENTIAL).

3 (POTENTIAL).

4 (POTENTIAL).

5 (POTENTIAL).

6 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MITOCHONDRION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Repeat; Transmembrane; Transport;
                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches 117; Indels 31; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   68223D27A0B4EFB0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 386;
                                                                                                                                                                                                                                                                                                                 292
                                                                                                                                                                                                                255
                                                                                                                                                                                                                                                                                                                                                                                                                  7;
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Qy

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                             Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Perfect score:
                                                                                                                                                                                                                                                                                  Database :
                                                                                                                                                                                                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Run on:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence:
SPTREMBL_19:*

Sp_archea:*

sp_archea:*

sp_bacteria

sp_fungi:*

4: sp_human:*

sp_human:*

sp_mamma?

7: sp_mamma?

7: sp_mhc:*

8: sp_orga

9: sp_pha/

10: sp_p)

11: sp_r

12: sp_p

14: sp

15: sp

16: sp

17:
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Gapop 10.0 , Gapext 0.5
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2481
1 MLRWLRDFALPTAACQDAEQ......VGISYVVYENMKQTLGVTQK 477
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         562222 seqs, 172994929 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
     sp_vertebrate:*
sp_unclassified:*
sp_rvirus:*
sp_bacteriap:*
sp_archeap:*
                                                                                 sp_plant:*
sp_rodent:*
sp_virus:*
                                                                                                                                                                                                                                              sp_archea:*
sp_bacteria:*
                                                                                                                                                    sp_organelle:*
                                                                                                                                                                                                   sp_invertebrate:*
                                                                                                                                                                                                                                                                                                                                                                                                                            562222
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

16	15	14	13	12	11	10	9	80	7	6	υī	4	ω	2	1	Result No.
520	520	521	612.5	652	840	852	885.5	902	1110	1285	1397	1487	1518	2132	2373	Score
21.0	21.0	21.0	24.7	26.3	33.9	34.3	35.7	36.4	44.7	51.8	56.3	59.9	61.2	85.9	95.6	Query Match Length DB
332	322	352	545	631	478	479	487	370	311	482	384	568	473	411	475	ength D
10	10	10	ω	w	10	10	10	U	4	4	4	4	11	4	6	. . .
Q9M058	Q9FU82	004619	Q96US1	Q9HE62	Q9FLS8	Q9LY28	Q9FI43	Q9VTX3	Q9BSA6	Q9BV35	Q96NQ4	Q96PZ1	Q9D5G5	Q9P129	018757	ID
Q9m058 arabidopsis	Q9fu82 oryza sativ	004619 arabidopsis	Q96us1 saccharomyc	Q9he62 neurospora	Q9fls8 arabidopsis	Q9ly28 arabidopsis	Q9fi43 arabidopsis	Q9vtx3 drosophila	Q9bsa6 homo sapien	homo	homo	Q96pzl homo sapien	Q9d5g5 mus musculu	Q9p129 homo sapien	018757 oryctolagus	Description

Query Match 95.6%; Score 2373; DB 6; Best Local Similarity 95.2%; Pred. No. 3.7e-170; Matches 454; Conservative 12; Mismatches 9;

Length 475; Indels

2; Gaps

1;

4 4 4 5	4 2	41	40	39	38	37	36	<u>3</u> 5	34	<u>3</u> 3	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17
356 355.5	357.5	360	362.5	365	367	367.5	368	369	371	400.5	•	417.5		429.5	434.5	445.5	446	446	448	448	454.5	455.5	462	475	500.5	506
14.3	14.5	14.5		14.7	14.8		14.8		15.0	16.1	16.5	16.8	17.2	17.3	17.5	18.0	18.0	18.0	18.1	18.1	18.3	18.4	18.6		20.2	20.4
301 315	346	298	334	298	298	348	298	339	298	319	377	326	418	294	428	381	392	385	325	316	381	415	126	348	426	358
4 5	10	13	10	4	13	10	13	10	13	10	5	ω	10	IJ	10	10	10	10	10	5	10	10	11	10		10
026006 09н0С2	Q25692 O9LIF7	0919M9	094222	Q96C49	Q9YIC4	Q9LJX5	Q9PRH2	Q9F173	Q9PRH1	Q9MA27	Q9VDL7	Q12251	Q9C9R4	Q93717	Q9LV81	Q9LD54	Q9SUV1	Q9ZNY4	Q9SZ19	Q9NI37	065023	Q9M024	Q99KD3	Q9SH98	094502	Q9M333
	Q25692 plasmodium O9lif7 arabidopsis	9	N	Q96c49 homo sapien	Q9yic4 rana ruqosa	Q9ljx5 arabidopsis		-		Q9ma27 arabidopsis		Q12251 saccharomyc	Q9c9r4 arabidopsis	C					Q9szi9 arabidopsis	Q9ni37 trichomonas		Q9m024 arabidopsis		Q9sh98 arabidopsis	co	Q9m333 arabidopsis

ALIGNMENTS

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Q9P129;
Q9P129;
Q1-OCT-2000 (TrEMBLrel. 15, Cr
Q1-OCT-2000 (TrEMBLrel. 15, La
Q1-DEC-2001 (TrEMBLrel. 19, La
C1-DEC-2001 (TREMBLREL 19, La
                                                       Query Match
Best Local
                                             Matches
                                                                                                                                                       Submitted (JAN-1999) to the EMBL/GenBa EMBL; AF123303; AAF28888.1; -. HSSP; P09860; SCIN. InterPro; IPR002048; EF-hand. InterPro; IPR001933; Mitcoh_carrier. InterPro; IPR002037; Mit_carrier. IPR002067; Mit_carrier. Pf6m; PF00153; mito_carr; 2.
                                                                                                                         PROSITE;
                                                                                                                                   PRINTS; PR00926; MITOCARRIER. SMART; SM00054; EFh; 3.
                                                                                                                                                                                                                                    "Cloning and subcellular localization transporter.";
                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                     TISSUE=RETINA;
                                                                                                                                                                                                                                                                                 SEQUENCE FROM
                                                                                                                                                                                                                                                                                             NCBI_TaxID=9606;
[1]
                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human).
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TAQTFIYPMEVMKTRLAVGKTGQYSGIYDCAKKILKHEGLGAFYKGYVPNLLGIIPYAGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISEQQAELILQSIDADGTMTVDWNEWRDYFLFNPVADIEEIIRFWKHSTGIDIGDSLTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISEQQAELILQSIDVDGTMTVDWNEWRDYFLFNPVTDIEEIIRFWKHSTGIDIGDSLTI 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EKIFTTGDVNKDGKLDFEEFMKYLKDHEKKMKLAFKSLDKNNDGKIEASEIVQSLQTLGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TAQTFIYPMEVMKTRLAVGKTGQYSGIYDCAKKILKYEGFGAFYKGYVPNLLGIIPYAGI 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MIKEGGVRSLWRGNGTNVIKIAPETAVKFWVYEQYKKLLTEEGQKIGTFERFISGSMAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PDEFTEEERKSGQWWRQLLAGGIAGAVSRTSTAPLDRLKVMMQVHGSKS--MNIFGGFRQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PDEFTEDEKKSGQWWRQLLAGGIAGAVSRTSTAPLDRLKIMMQVHGSKSDKMNIFGGFRQ
                                                                                                                                                                                                                                                           B., Valle D.;
                                                        Similarity
                                                                                                                         PS00018;
                                           Conservative
                                                                                                                                                                                                                                                                               N.A.
                                                                                                    ΑĄ,
                                                                                                                        EF_HAND; UNKNOWN_3.
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Last annotation updat
(FRAGMENT).
                                          Score 2132; I
Pred. No. 4e-1
0; Mismatches
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RESULT
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A Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
A Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
A Arakawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
A Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
A Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
A Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
A Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
A Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
A Schrimi L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
A Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
A Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
A Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
A Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
A Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
A Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
A Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.

RA Winshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                    EMBL; AK015371; BAB29816:1; -.
HSSP; Q64537; 1DVI.
HSSP; Q64537; 1DVI.
InterPro; IPR002048; EF-hand.
InterPro; IPR001993; Mitoch_carrier.
InterPro; IPR001993; Mitcarrier.
InterPro; IPR002067; Mit_carrier.
Pfam; PF00153; mito_carr; 3.
PROSITE;
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUN-2001 (TrEMBLrel.
01-JUN-2001 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
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4930443G12RIK.
                                                     PRINTS; PR00926; MITOCARRIER. SMART; SM00054; EFh; 4.
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Hayashizaki Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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Mammalia; Eutheria; Rodentia;
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'6J; TISSUE=TESTIS;
5660; PubMed=11217851;
chibata K.
; EF_HAND;
A; 53375 N
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Sciurognathi; Muridae;
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Q96PZ1;
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01-DEC-2001 (TrEMBLrel. 19, L¢
01-DEC-2001 (TrEMBLrel. 19, L¢
KIAA1896 PROTEIN (FRAGMENT).
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Homo sapiens (Human).
Thervota; Metazoa; Chordata;
Theria; Primates;
                                                                                                                                                                                                                                                                       Nagase T., Kikuno R., Ohara O.;
"Prediction of the coding sequences
The complete sequences of 60 new cDl
large proteins."
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Best Local
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Q1-DEC-2001 (TrEMBLrel. 19, Created)
Q1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
Q1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Q1-DEC-2001 (TrEMBLrel. 19, Cast annotation update)
Q1-DEC-2001 (TrEMBLrel. 19, Created)
Q1-DEC-2001 (TrEMBLrel. 19, Created)
Q1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
Q1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Q1-DEC-2001 (Tr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tashiro H., Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y., Fujimori Y., Komiyama M., Sugiyama T., Irie R., Otsuki T., Sato H., Wakanatsu A., Ishi S., Yamamoto J., Isono Y., Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H., Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagatsuma Murakawa K., Kanehori K., Takahashi-Fujii A., Oshima A., Sugiyama A. Kawakami B., Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K. Isogai T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "NEDO human cDNA sequencing project."; Submitted (OCT-2001) to the EMBL/GenBank/DDBJ EMBL; AK054901; BAB70825.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human),
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Euthoria; Primates; Catarrhini; Hominidae;
NCBI_TaxID-9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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Pred. No. 6.8e-97;
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Q1-JUN-2001 (TrEMBLrel. 17, La
Q1-DEC-2001 (TrEMBLrel. 19, La
HYPOTHETICAL 54.0 KDA PROTEIN.
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InterPro; IPR001993; Mitoch_carrier.
InterPro; IPR002067; Mit_carrier.
Pfam; PF00153; mito_carr; 2.
PRINTS; PR00926; MITOCARRIER.
SMART; SM00054; EFh; 3.
                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=EYE, RES
                                                                                                                                                                                                                                                                       Hypothetical protein.
SEQUENCE 482 AA; 54035 MW;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Local Similarity
Les 242; Conserv
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                    AVSRTSTAPLDRLKIMMQVHGSKSDKMNIFGGFRQMVKEGGIRSLWRGNGTNVIKIAPET
                                        TVLARRSGSHLKSQHFGRPKWADHEVLDIGECLTVPDEFSKQEKLTGMWWKQLVAGAVAG
                                                                                      SMDRDGTMTIDWQEWRDHFLLHSLENVEDVLYFWKHSTLSSAGFSAWIKDSTAEQNRSKT
                                                                                                 SIDVDGTMTVDWNEWRDYFLFNPVTDIEEIIRFWKHST
                                                                                                                               GGLDLEEFSRYLQEREQRLLLMFHSLDRNQDGHIDVSEIQQSFRALGISISLEQAEKILH
                                                                                                                                                   GKLDFEEFMKYLKDHEKKMKLAFKSLDKNNDGKIEASEIVQSLQTLGLTISEQQAELILQ 132
                                                                                                                                                                          DAERRQRWGRLFEELDSNKDGRVDVHELRQGLARLG---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SSTCGQLASYPLALVRTRMQAQAMLEGSPQLNMVGLFRRIISKEGIPGLYRGITPNFMKV
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                                                                                                                                                                                                                                                                                           PS00018; EF_HAND; UNKNOWN_2
                                                                                                                                                                                                                                                                                                                                                                                                        RETINOBLASTOMA;
                                                                                                                                                                                                                     Conservative
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Last annotation update)
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Pred.
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Best Local S
Matches 203
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01-JUN-2001
01-JUN-2001
01-DEC-2001
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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01-JUN-2001 (TrEMBLrel. 17, Last sequence
01-DEC-2001 (TrEMBLrel. 19, Last annotati.
HYPOTHETICAL 34.0 KDA PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (MAR-2001) to the EMBL/GenBank/DDBJ EMBL; BC005163; AAH05163.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PR00926; MITOCARRIER.
PROSITE; PS00215; MITOCH_CARRIER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR001993; Mitoch_carrier
InterPro; IPR002067; Mit_carrier.
Pfam; PF00153; mito_carr; 3.
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TISSUE=MUSCLE, RHA
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307
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                                                                                                                              413
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                                                                                                                                                                                                                                                                                                                                                                                                                                          GIIPYAGIDLAVYELLKSYWLDNFAKDSVNPGVMVLLGCGALSSTCGQLASYPLALVRTR 412
                                                                                                                                                                                                                                                                                     ISGSMAGATAQTFIYPMEVMKTRLAVGKTGQYSGIYDCAKKILKHEGLGAFYKGYVPNLL::||:|| || ||:|| ||:||
                                                                                                                                                                                                                                                                                                                                                                          NIFGGFROMVKEGGIRSLWRGNGTNVIKIAPETAVKFWAYEQYKKLLTEEGQKIGTFERF
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                                       GVTQK 477
                                                                                                                                                                            GIIPYAGIDLAVYETLKNAWLQHYAVNSADPGVFVLLACGTMSSTCGQLASYPLALVRTR
                                                                                                                                                                                                                                                              VAGSLAGAIAQSSIYPMEVLKTRMALRKTGQYSGMLDCARRILAREGVAAFYKGYVPNML
                                                                                                                                                                                                                                                                                                                                                   GIVGGFTQMIREGGARSLWRGNGINVLKIAPESAIKFMAYEQIKRLVGSDQETLRIHERL 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 203;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity 66.003; Conservative
  311
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               51;
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Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 1110; DB 4;
Pred. No. 1.9e-75;
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RESULT Q9VTX3

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RA Adams M.D., Celniker S.E., Helt R.A., Evans C.A., Golayne J.D.,
RA Adams M.D., Celniker S.E., Helt R.A., Evans C.A., Galle R.F.,
RA Adams M.D., Celniker S.E., Helt R.A., Evans C.A., Galle R.F.,
RA Adams M.D., Celniker S.E., Helt R.A., Evans Q., Chen L.X.,
RA Burton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Burdon R.C., Rogers Y.H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Beson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Beson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Glabar W.M., Glasser K.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Ketchum K.A.,
RA Harris N., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Nelson D.L.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Syirakas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Sillams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Wang X., Yeh R., F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
The genome sequence of Drosophila melanogaster ";
Science 287:2185-2195(2000)
                                                                Query Match
Best Local S
Matches 182
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Pterygota;
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Q9VTX3;
01-MAY-2000
01-MAY-2000
01-OCT-2001
                                                                                                                                                                                                                                                            PlyBase; FBgn0036283; CG4392.
InterPro; IPR001993; Mitoch_carrier.
InterPro; IPR002067; Mit_carrier.
Pfam; PF00153; Mito_carr; 3.
PRINTS; PR00926; MITOCARRIER.
PROSITE; PS00215; MITOCH_CARRIER; 1.
                                                                                                                                                                                                              SEQUENCE 370
                                                                                                                                                                                                                                                                                                                                                                                                                                               -i- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL INNER MEMBRANE (BY SIMILARITY).
-i- SIMILARITY: BELLONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
EMBL; AE003541; AAF49922.1; -.
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            159
IEEIIRFWKHSTG--IDIGDSLTIPDEFTEDEKKSGQWWRQLLAGGIAGAVSRTSTAPLD 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROTEIN.
                                                                                            Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 melanogaster (Fruit fly).
Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (TrEMBLrel. 13, (TrEMBLrel. 13, (TrEMBLrel. 18,
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                                                                                                                                                                                                              AA; 41539 MW;
                                                                                         36.4%;
                                                             58;
                                                       Score 902; DB
Pred. No. 1.1e
58; Mismatches
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Last annotation update
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                                                                                                                                                                                                           Transmembrane; T: 9A4F1BA9A9E5CCE1
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                                                          DB 5; 1
1.1e-59;
nes 75;
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                                                                                                                                                                                                        Transport.
El CRC64;
                                                                                                               Length 370;
                                                             Indels
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Best Local Similarity
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Q9FI43;
                                                                                                                                                                                                                                                InterPro; IPR002048; EF-hand.
InterPro; IPR001993; Mitoch_carri
InterPro; IPR002067; Mit_carrier.
Pfam; PF00153; Mito_carr; 3.
PRINTS; PR00926; MITOCARRIER.
SMART; SM00054; EFh; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arabidopsis thaliana (Mouse-ear cress)...
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosideurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence up
01-DEC-2001 (TrEMBLrel. 19, Last annotation
CALCIUM-BINDING TRANSPORTER-LIKE PROTEIN.
                                                                                                                                                                                                                                                                                                                                              P1 and TAC clones.";
DNA Res. 6:183-195(1999).
EMBL; AB017063; BAB08751.1;
                                                                                                                                                                                                                                                                                                                                                                                      Kaneko T., Katoh T., Sato S., Nakamura Y., Asamizu E., F
Miyajima N., Tabata S.;
"Structural analysis of Arabidopsis thaliana chromosome
Sequence features of the regions of 1,011,550 bp covered
                                                                                                                                                                                                                        PROSITE; PS00018; SEQUENCE 487 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=COLUMBIA; PubMed=10470850; MEDLINE=99397451; PubMed=10470850;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                   HSSP; P09860; 1FI5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=3702;
               139
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                                         96
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                                                                                                                         19
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EQPTRYETLFQALDRNGDGVVDIGELQEGLRNLGIPLGQDAEEKIFTTGDVNKDGKLDFE
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                                         EFRRYMDDKELELYRIFQAIDVEHNGCISPEGLWDSLVKAGIEIKDEELARFVEHVDKDN
                                                                  EFMKYLKDHEKKMKLAFKSLDKNNDGKIEASEIVQSLQTLGLTISEQQAELILQSIDVDG
                                                                                               ERDLRIRSLFSFFDSENVGYLDCAQIEKGLCALQIPSGYKYAKELFRVCDANRDGRVDYH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EQYKKLL--TEEGQKIGTFERFISGSMAGATAQTFIYPMEVMKTRLAVGKTGQYSGIYDC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RLKIMMQVHGSK----SDKMNIFGGFRQMVKEGGIRSLWRGNGTNVIKIAPETAVKFWAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CGSTSSTLGQLCSYPLALVRTRLQAQAAETIANQKRKTQIPLKSSDAHSGEETMTGLFRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AVKIYKQEGVRSFYRGYVPNILGILPYAGIDLAVYETLKRRYIANH-DNNEQPSFLVLLA
                                                                                                                                                      190;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EQMKRLIRGDDGSRQMSIVERFYAGAAAGGISQTIIYPMEVLKTRLALRRTGQYAGIADA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RIKVYLQVNQPRYTVQTQRMGISECMHIMLNEGGSRSMWRGNGINVLKIAPETAFKFAAY
                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                          AA;
                                                                                                                                                                                                                        EF_HAND; UNKNOWN_1; 54505 MW; 2268B
                                                                                                                                                                35.7%;
                                                                                                                                                                                                                                                                                                        Mitoch_carrier.
                                                                                                                                                    ; 68
                                                                                                                                                                 Score 885.5; DB 1
Pred. No. 2.9e-58;
                                                                                                                                                                                                                        2268B650C8841537 CRC64;
                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ä
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                                                                                                                                                    156;
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                                                                                                                                                   Indels
                                                                                                                                                                             Length 487;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Kotani
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                                                                                                                                                   33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rosidae;
                                                                                                                                                   Gaps
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                                         155
                                                                   138
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197 152

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RESULT
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AC 09
AC 09
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                                                                                                                                                      Query Match
Best Local S
Matches 181
                                                                                                                                                                                                                                                                                                                                      C -!- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.

R EMBL; AL163912; CAB87921.1; -.

R InterPro; IPR002048; EF-hand.

R InterPro; IPR001986; EPSP_syntase.

R InterPro; IPR001993; Mitoch_carrier.

R InterPro; IPR001993; Mitoch_carrier.

R Pfam; pF00153; mito_carr; 3.

R PRINTS; PR00926; MITOCARRIER.

R PROSITE; PS00104; EFSP_SYNTHASE_1; UNKNOWN_1.

R PROSITE; PS00104; EPSP_SYNTHASE_1; UNKNOWN_1.

R PROSITE; PS00104; EPSP_SYNTHASE_1; UNKNOWN_1.
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01-OCT-2000
01-DEC-2001
                                                                                                                                                                                                                                                                                          Inner men
SEQUENCE
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Rudd (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EU Arabidopsis sequencing pr
Submitted (APR-2000) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta;

Spermatophyta; Magnoliophyta; Eudioctyledons; core eu
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (APR-2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 437
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         383
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              329
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        198
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        79
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INNER MEMBRANE (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LNMVGLFRRIISKEGIPGLYRGITPNFMKVLPAVGISYVVYENMKQTL
EFMKYLKDHEKKMKLAFKSLDKNNDGKIEASEIVQSLQTLGLTISEQQAELILQSIDVDG
                                                                                                     EQPTRYETLFQALDRNGDGVVDIGELQEGLRNLGIPLGQDAEEKIFTTGDVNKDGKLDFE
                                                                                                                                                            181;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TSMSGVFRRTISEEGYRALYKGLLPNLLKVVPAASITYMVYEAMKKSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YELLKSYWLDNFAKDSVNPGVMVLLGCGALSSTCGQLASYPLALVRTRMQAQAMLEGSPQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VIKIAPETAVKFWAYEQYKKL----LTEEGQKIGTFERFISGSMAGATAQTFIYPMEVMK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       - IAGGIAGAASRTATAPLDRLKVLLQI - -QKTD-ARIREAIKLIWKQGGVRGFFRGNGLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DGIIMFEEWRDFLLLYPHEATIENIYHHWERVCLVDIGEQAVIPEGISKHIKRSNYF---
                                                      EREIRIRSLFDFFDNSNLGFLDYAQIEKGLASLQIPPEYKYARDLFRVCDANRDGRVDYQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YETLKDLSRTYILQDA-EPGPLVQLGCGTISGALGATCVYPLQVVRTRMQAE---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TRLQTYTSQAGVAVPRLGTLT------KDILVHEGPRAFYKGLFPSLLGIIPYAGIDLAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IVKVAPESAIKFYAYELFKNAIGENMGEDKADIGTTVRLFAGGMAGAVAQASIYPLDLVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCE FROM N.A.
M., Murphy G., Ridley P.,
S., Lemcke K., Mayer K.F.X
                                                                                                                                                                                                                                                                                          membrane; Mitochondrion; NCE 479 AA; 53969 MW;
                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (TrEMBLrel. 15, Created)
(TrEMBLrel. 15, Last sequence update)
(TrEMBLrel. 19, Last annotation update)
CA-DEPENDENT SOLUTE CARRIER-LIKE PROTEIN
                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N.A.
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                                                                                                                                                                                  34.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                project;
he EMBL/GenBank/DDBJ
                                                                                                                                                            90;
                                                                                                                                                         Score 852; DB
Pred. No. 9.3e-
90; Mismatches
                                                                                                                                                                                                                                                                                          Transmembrane; Transport. 38D58E1395316D6E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hudson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            s,
                                                                                                                                                         DB 10;
).3e-56;
les 172;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     databases
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                                                                                                                                                                                                          Length
                                                                                                                                                            Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MITOCHONDRIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 484
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mewes
                                                                                                                                                         16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rosidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ξ.
                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Έ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          424
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RESULT QUELLE QU
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                                                                                                                                                                                                                                                 ramada K., Banh J., Banno F., Dale J.M., Goldsmith A.D., Lee J.M.
Onodera C.S., Quach H.L., Tang C., Toriumi M., Yamamura Y., Yu G.
Yu S., Bowser L., Carninci P., Chen H., Cheuk R., Hayashizaki Y.,
Ishida J., Jones T., Kamiya A., Karlin Neumann G., Kawai J., Kim (
Koesema E., Lam B., Lin J., Meyers M.C., Miranda M., Narusaka M.,
Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M., Shinn P.,
Southwick A., Tracy S.E., Shinozaki K., Davis R.W., Ecker J.R.,
Theologis A.;
"Firll towards"
                                                 InterPro; IPR002048; EF-hand.
InterPro; IPR001993; Mitoch_carrier.
InterPro; IPR002067; Mit_carrier.
Pfam; PF00153; mito_carr; 3.
                                                                                                                                                      Submitted (SEP-2001) to the EMBL/GenBank/DDBJ EMBL; AB010069; BAB10081.1; -. EMBL; AY056219; AAL07068.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Structural analysis of Arabidopsis thaliana c Sequence features of the regions of 1,456,315 physically assigned Pl and TAC clones."; DNA Res. 5:41-54(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=COLUMNIA
MEDLINE=98290546; Pu
Kaneko T.,
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01-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM
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Eukaryota; Viridiplantuae; Streptophyta; Embryophyta;

Spermatophyta; Magnollophyta; eudicotyledons; core eu

eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                                'Full Length cDNA of gene
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KGEGLRGFYRGLLPNLLKVVPAASITYIVYEAMKKNMAL 478
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16, Last sequence update)
19, Last annotation update)
19 CARRIER-LIKE PROTEIN
T SOLUTE CARRIER PROTEIN).
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Best Local S
Matches 180
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Q9HE62;
Q1-MAR-2001 (TrEMBLrel. 16, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
01-DEC-2001 (TREMBLREL. 19, Last annotation update)
                                                                                                                                                                                                              SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
Schulte U., Aign V., Hoheisel J., Brandt P., F
Schulte U., Aign V., Hoheisel J., Brandt P., F
Nyakatura G., Mewes H.W., Mannhaupt G.;
Nyakatura (DEC-2000) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE;
SEQUENCE
                                                                                                                                           German Neurospora genome project;
Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases
EMBL; AL451012; CAC18152.2; -.
                                                                                                                                                                                                                                                                                                         Neurospora crassa.
Eukaryota; Fungi; Ascomycot
Sordariales; Sordariaceae;
NCBI_TaxID=5141;
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478 AA;
                                                                                                                                 631 AA;
                                                     Conservative
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                                                                                                                                                                                                                                                                                                                           Ascomycota; Pezizomycotina; ariaceae; Neurospora.
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                                                                                                                                  68433 MW;
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                                              Score 652; DB
Pred. No. 1.6e
99; Mismatches
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Pred. No. 7.4e-55;
8; Mismatches 171;
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                                                                 .6e-40;
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Saccharomycetales;
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Belenkiy R., Wohlrab H.;
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ
EMBL; AF419344; AAL26493.1; -.
SEQUENCE 545 AA; 61270 MW; 8F33AA9AE392538
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PUTATIVE CARRIER PROTEIN (AT4G01100/F2N1_16).
A_IG002N01.16 OR AT4G01100.
Arabidopsis thalians '...
                                                                                                                                                                                          Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidieurosids_II; Brassicales; Brassicaceae; Arabidopsis.
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004619; PRELIMINARY;
01-JUL-1997 (TrEMBLrel. 04,
01-JUL-1997 (TrEMBLrel. 04,
01-DEC-2001 (TrEMBLrel. 19,
Lamar B., Stoneking Mayer K.F.X.; Submitted (MAR-2000)
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                                    SEQUENCE FROM N.
                                                                        Waterston
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EMBL; AF007269; AAB61037 1; -.
EMBL; AF161491; CAB80919 1; -.
EMBL; AF360168; AAK25878 1; -.
EMBL; AF4161481; AAL07192 1; -.
EMBL; AF412085; AAL06538 1; -.
EMBL; AF412085; AAL06538 1; -.
EMBL; AF412085; AAL06538 1; -.
InterPro; IPR001993; Mitoch_carrier.
InterPro; IPR001993; Mitoch_carrier.
Pfam; PF00153; Mito_carr; 3.
PRINTS; PR00926; MITOCARRIER.
PROSITE; PS00215; MITOCH_CARRIER; UNKN
SEQUENCE 352 AA; 38325 MW; 360CAA7
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"Full Length CDNA of gene AT4901100 (GI:7267607).";
"Full Length CDNA of gene AT4901100 (GI:7267607).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cheuk R., Chen H., Kim C.J., Koesema E., Meyers M.C., Banh J., Bowser L., Carninci P., Dale J.M., Goldsmith A.D., Hayashizaki Y., Ishida J., Jiang P.X., Jones T., Kamiya A., Karlin Neumann G., Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka Nguyen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K., Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M. Goldsmith A.D., Lee J.M., Quach H.L., Toriumi M., Yu G., Bow Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., J. Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    [4]
SEQUENCE FROM N.A.

EU Arabidopsis sequencing project;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
[5]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted [7]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Theologis A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seki M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ecker J.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Full Length cDNA
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   415
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                                                                                                                                                                                                                                                                                                     Local Similarity
nes 115; Conser
                                                                                                                                                                                        GTNVIKIAPETAVKFWAYEQ------
                                                                                                                                                                                                                                                      YPMDMVRGRLTVQTANSPYQYRGIAHALATVLREEGPRALYRGWLPSVIGVVPYVGLNFS
                                                                                                                YPMEVMKTRLAVGKTG---QYSGIYDCAKKILKHEGLGAFYKGYVPNLLGIIPYAGIDLA
                                                                                                                                                                   GTNCARIVPNSAVKFFSYEQASNGILYMYRQRTGNENAQLTPLLRLGAGATAGIIAMSAT
                                                                                                                                                                                                                                     KSLFAGGVAGGVSRTAVAPLERMKILLQVQNPHNIKYSGTVQGLKHIWRTEGLRGLFKGN
                                    VYESLKD
                                                                VYELLKSYWLDNFAKDSVNP-----
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   AQAMLEGSPQ-
                                                                                                                                                                                                                                                                                                     Conservative
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Quach H.L., Tang C., Toriumi
L., Carninci P., Chen H., Che
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                                  -VKE-
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                                                                                                                                                                                                                                                                                                                     21.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene AT4g01100 (GI:7267607).";
to the EMBL/GenBank/DDBJ databases
                                  NPYGLVENNELTVVTRLTCGAIAGTVGQTIAYPLDVIRRRMQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AT4g01100 (GI:7267607).";
he EMBL/GenBank/DDBJ datab
                                                                                                                                                                                                                                                                                                       64;
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 LNMVGLFRRIISKEGIPGLYRGITPNFMKVLPAVGIS
                                                                                                                                                                                                                                                                                                     Score 521; DB 10;
Pred. No. 4.6e-31;
4; Mismatches 94
                                                                                                                                                                                                                                                                                                                                                                                       ER; UNKNOWN_1.
360CA4785EFB4A8B
                                                                                                                                                                                                  -YKKLLTEEGQKIGTFERFISGSMAGATAQTFI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Shinozaki K., Davis R.W., Ecker
                                                                -GVMVLLGCGALSSTCGQLASYPLALVRTRMQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , Goldsmith A.D., Lee J.M., umi M., Yamamura Y., Yu G., Cheuk R., Hayashizaki Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Goldsmith A.D., I
                                                                                                                                                                                                                                                                                                       94;
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Bowser L.,
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n J.,
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Ecker J.R.,
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C STRAIN-CV NIPPONBARE;

A Sasaki T., Matsumotto T., Yamamotto K.;

A Correspondence of T., Yamamotto K.;

A Correspondence of T., Yamamotto K.;

Cone:P0024G09.";

Clone:P0024G09.";

Clone:P0024G09.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 117; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
PUTATIVE PEROXISOMAL CA-DEPENDENT SOLUTE CARRIER PROTEIN.
P0019D06.21 OR P0024G09.9.
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STRAIN=CV. NIPPONBARE;
Sasaki T., Matsumoto T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oryza sativa (Rice).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1,
clone:P0019D06.":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9FU82;
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GNGTNVIKIAPETAVKFWAYEQYKKL-----LTEEGQKIGTFERFISGSMAGATAQTFI 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LAAGGFAGAVSKTCTAPLARLTILFQVAGMHSDVAALKKYSIWHEASRIVREEGFGAFWK
                                                                                                                                         ESLRSHWQMERPQDS--PAVVSLFS-GSLSGIASSTATFPLDLVKRRMQLQGAAGTSSVC
                                                                                                                                                                                                                                                                                                                                     YPMEVMKTRLAVGKTGQ-YSGIYDCAKKILKHEGLGAFYKGYVPNLLGIIPYAGIDLAVY
                                                                                                                                                                          GNLVTIVHRLPYSAISFYSYERYKKFLQRVPGLDEDSNYVGV-ARLLSGGLAGITAASVT
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nilarity 40.5%;
Conservative 5:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 520; DB 10;
; pred. No. 4.7e-31;
51; Mismatches 103;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    103;
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Search completed: August 18, 2002, 09:30:28 Job time: 483 sec

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Database
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Maximum DB seq length: 2000000000
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Perfect score:
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1: //ggn2_6/ptodata/1/pna/US06_COMB.seq:*
2: //ggn2_6/ptodata/1/pna/US07_COMB.seq:*
3: //ggn2_6/ptodata/1/pna/US07_COMB.seq:*
4: //ggn2_6/ptodata/1/pna/US080_COMB.seq:*
5: //ggn2_6/ptodata/1/pna/US080_COMB.seq:*
6: //ggn2_6/ptodata/1/pna/US082_COMB.seq:*
7: //ggn2_6/ptodata/1/pna/US082_COMB.seq:*
8: //ggn2_6/ptodata/1/pna/US085_COMB.seq:*
9: //ggn2_6/ptodata/1/pna/US085_COMB.seq:*
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Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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Copyright (c) 1993 - 2000 Compugen Ltd.
/cgn2_6/ptcdata/1/pna/US092_COMB.seq:*
/cgn2_6/ptcdata/1/pna/US093_COMB.seq:*
/cgn2_6/ptcdata/1/pna/US093_COMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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26/3 35/45 35/45 35/45 35/45 35/45 35/45 35/45 34/46 3	
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US-09-7/7-921-1 US-09-649-163-8441 US-09-652-121-6793 US-09-652-121-9699 US-09-652-123-9699 US-09-652-131-9699 US-09-652-918-8162 US-09-698-010-12652 US-09-710-285-1759 US-60-213-360-3302 US-60-213-360-3302 US-60-213-561-2850 PCT-US01-44098A-755 PCT-US01-4827-2497 US-09-644-869-8718 US-09-644-869-8718 US-09-644-869-8718 US-09-644-869-8718 US-09-644-869-8718 US-09-644-869-8718 US-09-644-869-8718 US-09-644-869-8718 US-09-652-127-8091 US-09-652-301-54 US-09-359-922-4478 US-09-359-922-4478 US-09-359-922-4478 US-09-850-118-1544	ID
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RESULT 1
US-09-777-921-1
Sequence 1, Application US/09777921
GENERAL INFORMATION: et al
APPLICANT: MERKULOV et al
TITLE OF INVENTION: ISOLATED HUMAN TRANSPORT
TITLE OF INVENTION: NUCLEIC ACID MOLECULES
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: CL001103
CURRENT FILING DATE: 2001-07-02
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSEQ for Windows Version 4.0
EQ ID NO 1
LENGTH: 2673
TYPE: DNA
ORGANISM: Human
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PCT-US01-01302-60
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Sequence 410, App
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Sequence 60, App1
Sequence 95, App1
Sequence 95, App1
Sequence 97, App
Sequence 739, App
Sequence 731, App
Sequence 731, App
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RESULT 2
US-09-522-303-1193
Sequence 1193, Application US/09522303
GENERAL INFORMATION:
APPLICANT: Gearing, David P.
APPLICANT: Holtzman, Douglas A.
TITLE OF INVENTION: NUCLEIC ACID MOLECULES DERIVITLE OF INVENTION: HUMAN MAMMARY EPITHELIUM LIE
FILE REFERENCE: 1600.1086-001
CURRENT APPLICATION NUMBER: US/09/522,303
CURRENT FILING DATE: 2000-03-08
EARLIER APPLICATION NUMBER: 60/123,393
EARLIER FILING DATE: 1999-03-08
NUMBER OF SEQ ID NOS: 1353
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1193
LENGTH: 3537
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; TYPE: DNA
; ORGANISM: HOMO
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Pred. No. 0;
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RESULT 3

(US-09-649-163-8441)
(Sequence 8441, Application US/09649163)
(GENERAL INFORMATION:
APPLICANT: Holtzman, Douglas A.
APPLICANT: Galvin, Katherine A.
APPLICANT: Keiby, Kevin R.
APPLICANT: Kingsbury, Gillian A.
APPLICANT: Weich, Nadine S.
APPLICANT: Williamson, Mark
APPLICANT: Williamson, Mark
APPLICANT: Richardson, Jennifer
APPLICANT: Fraser, Christopher C.
APPLICANT: Villeval, Jean-Luc M.G.

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; ORGANISM: Homo sapiens
US-09-649-163-8441
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SOFTWARE: Fast
SEQ ID NO 8441
FRIGTH: 3545
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Best Local Similarity
Matches 2549; Conserv
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TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
TITLE OF INVENTION: THEREFOR
FILE REFERENCE: 1600.1164-001
CURRENT APPLICATION NUMBER: US/09/649,163
CURRENT FILING DATE: 2000-08-25
PRIOR APPLICATION NUMBER: 60/150,608
PRIOR FILING DATE: 1999-08-25
PRIOR FILING DATE: 1999-08-25
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Silos-Santiago, Inmaculada
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1740	cacaaaagggaagacggtaacaatggtcacttcaaacttttgggctaaattatatgtaca	1681	Qy
1785		1726	Db
1680	ggagtgactttttctcctcgaattgaaacaagtctatggcaaaagaagctgcattttttt	1621	Qy
1725		1666	Db
1620	cccagaaatgatgttgcattttttgctttagcctgataattgaaactttcaacaatctct	1561	Qy
1665		1606	Db
1560	tccctgctgtaggcatcagttatgtggtttatgaaaatatgaagcaaactttaggagtaa	1501	Qy
1605		1546	Db
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840	tggaccgtctgaaaatcatgatgcaggttcacggttcaaaatcagacaaaatgaacatat	781	Qy
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US-09-652-121-6793

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RESULT 4
US-09-652-121-6793
; Sequence 6793, Application US/09652121
; GENERAL INFORMATION:
; APPLICANT: DIStefano, Peter
; TITLE OF INVENTION: NOVEL NUCLEIC ACID
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 1600.1188-001
; CURRENT APPLICATION NUMBER: US/09/652,12
; CURRENT FILING DATE: 2000-08-30
; CURRENT FILING DATE: 2000-08-30
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             PRIOR APPLICATION NUMBER: (PRIOR FILING DATE: 1999-08: NUMBER OF SEQ ID NOS: 7615: SOFTWARE: FastSEQ for Windc; SEQ ID NO 6793: LENGTH: 3545
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TYPE: DNA
ORGANISM: Homo
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Sequence 9069, APPL.

GENERAL INFORMATION:

APPLICANT: HOLTZMAN, DOUGLAS A.

APPLICANT: HOLTZMAN, OVEL NUCLEIC ACID MO
TITLE OF INVENTION: THEREFOR
FILE REFERENCE: 1600.1186-001
CURRENT APPLICATION NUMBER: US/09/652,12?
CURRENT FILING DATE: 2000-08-30
PRIOR APPLICATION NUMBER: 60/151,135
PRIOR FILING DATE: 1999-08-30
NUMBER OF SEQ ID NOS: 9796
NUMBER OF SEQ ID NOS: 9796
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; ORGANISM: Homo
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Best Local Similarity 99.3%;
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APPLICANT: Galvin, Katherine
APPLICANT: Holtzman, Douglas A.
FITLE OF INVENTION: MOVEL NUCLEIC ACID MOLE
CURRENT APPLICATION: THEREFOR
CURRENT APPLICATION NUMBER: US/09/652,918
CURRENT FILING DATE: 2000-08-30
PRIOR APPLICATION NUMBER: 60/151,130
PRIOR APPLICATION NUMBER: 60/151,130
PRIOR FILING DATE: 1999-08-30
VUMBER OF SEQ ID NOS: 8985
SOFTWARE: FASTSEQ for Windows Version 4.0
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ORGANISM: Homo
S-09-652-918-8162
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GENERAL INFORMATION:
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RESULT 7
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; Sequence 1724, Application U
; GENERAL INFORMATION:
APPLICANT: Holtzman, Dougl
; APPLICANT: Gearing, David
; TITLE OF INVENTION: NOVEL
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; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 1600.1198-001
; CURRENT APPLICATION NUMBER: US/99/667,61
; CURRENT FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: 60/155,295
; PRIOR FILLING DATE: 1999-09-21
; NUMBER OF SEQ ID NOS: 2254
; SOFTWARE: FRASESEQ for Windows Version 4
; SEQ ID NO 1724
; SEQ ID NO 1724
; LENGTH: 3545
; TYPE: DNA
; ORGANISM: Homo sapiens
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CURRENT APPLICATION NUMBER: US/09/698,01
CURRENT FILING DATE: 2000-10-27
PRIOR APPLICATION UNBER: 600/162,358
PRIOR FILING DATE: 1999-10-29
NUMBER OF SEQ ID NOS: 15684
SOFTWARE: FastSEQ for Windows Version 4
SEQ ID NO 12652
LENGTH: 3545
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                                   LENGTH: 3545
TYPE: DNA
ORGANISM: Homo sa
Query Match
Best Local Similarity 99.3
Matches 2549; Conservative
                                                                                                                                                        Sequence 12652, Application GENERAL INFORMATION:
                                                                                                                    APPLICANT: Williamson, Mark
APPLICANT: Shyjan, Andrew W.
TITLE OF INVENTION: NOVEL NUCLEIC
TITLE OF INVENTION: THEREFOR
FILE REFERENCE: 1600.2029-001
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Score 2517.4;
Pred. No. 0;
0; Mismatches
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APPLICANT: Gearing, David P.
APPLICANT: Donovan, Michael J.
APPLICANT: Holtzman, Douglas A.
TITLE OF INVENTION: NOVEL NUCLEIC ACID P.
TITLE OF INVENTION: THEREFOR
FILE REFERENCE: 1600.2006-001
CURRENT APPLICATION NUMBER: US/09/710,289
CURRENT FILING DATE: 2000-11-10
PRIOR APPLICATION NUMBER: 60/164,507
PRIOR FILING DATE: 1999-11-10
NUMBER OF SEQ ID NOS: 2347
SOFTMARE: FastSEQ for Windows Version 4.
SEQ ID NO 1759
TYPE: DNA
CORGANISM: Homo sapiens
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SOFTWARE: FastSEQ I
SEQ ID NO 3387
LENGTH: 3545
TYPE: DNA
TYPE: DNA
CRGANISM: Homo sapi
US-09-726-810-3387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Gearing, David P.
APPLICANT: Holtzman, Douglas A.
TITLE OF INVENTION: NOVEL NUCLEIC ACID
TITLE OF INVENTION: THEREFOR
FILE REFERENCE: 1600.2016-001
CURRENT APPLICATION NUMBER: US/09/726,81
CURRENT FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: 60/18,017
PRIOR APPLICATION NUMBER: 1099-11-30
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Best Loc
Matches
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US-00-213-360-3302

Sequence 3302, Application US/60213360

GENERAL INFORMATION:

APPLICANT: MORYIS, MacDonald

APPLICANT: Lal, Preeti

APPLICANT: Diep, Dinh

TITLE OF INVENTION: Method for the Identi

TITLE OF INVENTION: Polynucleotide Sequer

TITLE OF INVENTION: Identified Thereby

FILE REFERENCE: GX-0014 p

CURRENT APPLICATION NUMBER: US/60/213,360

CURRENT APPLICATION NUMBER: US/60/213,360
                                 US/60/213,360
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TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KBY: misc_feature
OTHER INFORMATION: Incyt
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SOFTWARE:
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APPLICANT: Ltal, Preet1
APPLICANT: Ltal, Preet1
TITLE OF INVENTION: METHOD FOR THE IDE
TITLE OF INVENTION: POLYMOREPHISMS IDE
TITLE OF INVENTION: POLYMORPHISMS IDE
TITLE REFERENCE: GX-0019-1 P
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Matches
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CURRENT FILING DATE: 2001-09-21
NUMBER OF SEQ ID NOS: 35862
SOFTWARE: PERL Program
SEQ ID NO 14440
LENGTH: 3446
                                                                                                                                                                                                                                                                                                      Sequence 14440, Application US/60324185 GENERAL INFORMATION:
                                                                                                            ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte
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APPLICANT: Norris, MacDonald

APPLICANT: Lal, Preeti

APPLICANT: Diep, Dinh

APPLICANT: Diep, Dinh

TITLE OF INVENTION: Method for the Identific

FILE REFERENCE: GX-0007 p

CURRENT APPLICATION NUMBER: US/60/172,360

CURRENT FILING DATE: 1999-12-16

NUMBER OF SEQ ID NOS: 29838

SOFTWARRE: PERL Program

SEQ ID NO 23662

LENGTH: 3393

TYPE: DNA

ORGANISM: Homo sapiens
FEARURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No: 221299.1

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Best Local Similarity 99.1
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RESULT 14
US-60-278-561-5850
; Sequence 5850, Application US/60278561
; GENERAL INFORMATION:

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; APPLICANT: Morris, MacDonald
; APPLICANT: Lal, Preeti
; APPLICANT: Diep, Dinh
; TITLE OF INVENTION: Method for the Iden
; TITLE OF INVENTION: Polynucleotide Set
; TITLE OF INVENTION: Polynurphisms Iden
; TITLE OF INVENTION: Polymorphisms Iden
; TITLE OF INVENTION: Morrisms Iden
; TITLE OF INVENTION: UNMBER: US/60/278,
CURRENT APPLICATION NUMBER: US/60/278,
CURRENT FILING DATE: 2001-03-23
; NUMBER OF SEQ ID NOS: 15598
; SOFTWARE: PERL PROGram
; SEQ ID NO 5850
; SEQ ID NO 5850
; TYPE: DNA
TYPE: DNA
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NAME/KEY: misc_feature
OTHER INFORMATION: Incyts-60-278-561-5850
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1681 1800 1501 1620 1561 1680 1621 1440 1381 1500 1441 1380

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Sequence 755, Application PC/TUS0104098A
GENERAL INFORMATION:
APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: NOVEL Nucleic Acids and Po
FILE REFERENCE: 21272-029
CURRENT APPLICATION UNMBER: PCT/US01/04098A
CURRENT FILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: Not Yet Assigned
PRIOR FILING DATE: 20001-01-30
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: 09/728,422
PRIOR APPLICATION NUMBER: 09/69,325
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-09-15
PRIOR APPLICATION NUMBER: 09/654,936
PRIOR APPLICATION NUMBER: 09/654,936
PRIOR APPLICATION NUMBER: 09/654,936
PRIOR APPLICATION NUMBER: 09/620,325
PRIOR APPLICATION NUMBER: 09/620,325
PRIOR FILING DATE: 2000-09-01
PRIOR APPLICATION NUMBER: 09/620,325
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: 09/560,875
PRIOR FILING DATE: 2000-04-27
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PRIOR APPLICATION NUMBER: 09/560,875

PRIOR FILING DATE: 2000-04-27

PRIOR FILING DATE: 2000-04-27

PRIOR FILING DATE: 2000-02-03

NUMBER OF SEQ ID NOS: 419

SEQ ID NO 408

LENGTH: 3384

TYPE: DATE: 2000-02-03
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APPLICANT: Tillinghast, John
APPLICANT: Dranac, Radoje T.
TITLE OF INVENTION: Novel Nucleic Acids ;
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 787CIP2B
CURRENT APPLICATION UNMER: US/09/620,32;
CURRENT FILING DATE: 2000-04-27
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NAME/KEY: CDS
LOCATION: (113)..(1546)
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Ren, Feiyan
Chen, Rui-hong
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Sequence 3. Application:

GENERAL INFORMATION:

APPLICANT: MERKULOV et al.

TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,

TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRAN

TITLE OF INVENTION: AND USES THEREOF

FILE REFERENCE: CLOO1103

CURRENT APPLICATION UNMBER: US/09/777,921A

CURRENT APPLICATION UNMBER: US/09/777,921A

CURRENT FILING DATE: 2002-02-07

NUMBER OF SEQ ID NOS: 126

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 3

LENGTH: 69327
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; LOCATION: (1)...(69327)
; OTHER INFORMATION: n = US-09-777-921A-3
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Best Local Similarity 98.6
Matches 1166; Conservative
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Pred. No. 4.3e-223;
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US-09-19-002-4478
; Sequence 4478, Application US/09919002
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                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/919,002
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: APPLICATION NUMBER: 09/359,922
PRIOR FILING DATE: FILING DATE: 1999-07-22
PRIOR APPLICATION NUMBER: APPLICATION NUMBER: US 09/034,3
PRIOR FILING DATE: FILING DATE: 1998-02-13
NUMBER OF SEQ ID NOS: 13203
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 4478
                                               Matches
                                                         Query Match
Best Local
                                                                                                  ORGANISM: Homo
-09-919-002-4478
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APPLICANT: Liu, Jin
TITLE OF INVENTION: NOVEL CONTIGS OBTAINED FROM
TITLE OF INVENTION: LIBRARIES
FILE REFERENCE: 20411-752CON1
                                                                                                                    SEQ ID NO 4478
LENGTH: 1839
TYPE: DNA
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                                              1 Similarity
976; Conserv
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ilarity 98.1%;
Conservative
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                                            Score 933.4; DB 5;
Pred. No. 4.1e-182;
0; Mismatches 16;
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Sequence 38, Application US/1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic
FILE REFERENCE: PJZ05C1
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P 29	1634 61	CTCCTCGGAATTGGAAGCAGGTCTAATGGCAAAAGAGGTGCA-TTTTTTTTTT
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Дb	121	atggtaacaatggtcacttcaaacttttgggctaaattatatgtacacagaaatgttc
Qy	1753	aatcatagttttaatgtgttttgaaaaggccacacaattatactttatctttctt
DЬ	181	aaatcatagttttaatgtgttttgaaaaggccacacaattatactttatctttctt
Qy	1813	atcctgcaaatctctgccctgaatccgaaatctgaaaatgtactggcttgaacaaat
DЬ	241	aatcctgcaaatctctgccctgaatcccgaaatctgaaaatgtactggcttgaacaaaatt 300
Qy	1873	gttttgtgtgttagagttataaatcattaatctttatttcgggtggtttacgtttatg
Db	301	ttgtgtgttagagttataaatcattaatctttatt
Qy	1933	agttcctttatatttaaatttcttgttttatatattttgaatgtctttatagatttct
DЪ	361	cagttcctttatatttcatatttcttgttttatatatttttgaatgtctttatagatttctt 420
Qy	1993	asatttoottatagaaccattaatagaaaatcattacatttaaaatataccttacagc
рь	421	taaatttccttatagaaccattaatagaaaatcattacatttaaaatataccttacagca 480
Qy	2053	nagcatccaaataagtatagggtttatgtccttatttttctttc
Db	481	aaagcatccaaataagtatagggtttatgtccttattttctttc
Qy	2113	ggtggaatttctgaagggaagtgatgaaattatatttatt
Db	541	gcacagtggtggaatttctgaagggaagtgatgaaattatttat
Qy	2173	taccattatttggttcctggagttatacactaattttca
Db	601	tccattttaccactgtaccattatttggttcctggagttatacactaattttcagta
Qy	2233	ctgttaaattaccaacacaaggcaatttatttgaaagattccgtttatcctgcca
Ф	661	tactgttaaattaccaacacaaggcaatttatttgaaagattccgt
Qy	2293	ctttgaaaagcagcaggaaacgaaatttttttgacttgtatcagcttctgcagagcat
Db	721	gct
Qy	2353	ttttcctttgtcctttgtttcctaccttttgaatcagattccgttttagtcagga
Db	781	ttgctttcctttgtcctttgtt
Qу	2413	acttcttgggaccattcttagtaacctgaaatttcttttttaattgcatgaagtggat
Db	841	gacttcttgggaccattcttagtaacctgaaatttcttttttaattgcatgaagtggatt 900
Qy	2473	atcatgagcaagtgatgggctttatttctccctcactggtgaatatcctttgaacttg
ф	901	gatcatgagcaaatgatgtgc-ttatttctccctcactgttgaatat-ctttgaacttgc 958
ОУ	2533	gtttgcaatatgggcagccacaaagggggagag
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NUMBER OF SEQ ID NOS: 384
SOFTWARE: PatentIn ver. 2.0
SEQ ID NO 38
LENGTH: 757
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LOCATION: (756)
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10-158-057-38
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NAME/KEY: misc_feature
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Pred. No. 1.4e
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GENERAL INFORMATION:
APPLICANT: MERKULOV et al.
TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUM
TITLE OF INVENTION: AND USES THEREOF
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SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 120
LENGTH: 601
TYPE: DNA
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Best Local Similarity
Matches 598; Conserv
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CURRENT APPLICATION NUMBER:
CURRENT FILING DATE: 2002-0
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2002-02-07
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: MERKULOV et al.
TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: CLOO1103
CURRENT APPLICATION NUMBER: US/09/777,921A
CURRENT FILING DATE: 2002-02-07
NUMBER OF SEQ ID NOS: 126
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 121
LENGTH: 601
TYPE: DNA
ORGANISM: Homo sapiens
US-09-777-921A-121
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Pred. No. 3.3e-113;
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CURRENT FILING DATE: 2002-05-20
PRIOR APPLICATION NUMBER: 09/866,050
PRIOR FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: 60/221,232
PRIOR APPLICATION NUMBER: 60/221,232
PRIOR APPLICATION NUMBER: 60/206,650
PRIOR FILING DATE: 2000-05-24
PRIOR PRICING DATE: 1990-05-14
PRIOR APPLICATION NUMBER: 09/312,283
PRIOR APPLICATION NUMBER: 09/312,283
PRIOR APPLICATION NUMBER: 09/312,930
PRIOR FILING DATE: 1999-04-29
PRIOR APPLICATION NUMBER: 09/188,930
PRIOR FILING DATE: 1998-11-09
PRIOR APPLICATION NUMBER: 09/069,726
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US-10-152-661-454
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Pred. No. 2.2e-102;
0; Mismatches 436;
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RESULT 9
US-09-312-283B-262
US-09-312-283B-262
Sequence 262, Application US/09312283B
GENERAL INFORMATION:
APPLICANT: Watson, James D.
APPLICANT: Strachan, Lorna
APPLICANT: Steeman, Matthew
APPLICANT: Onrust, Rene
APPLICANT: Murison, James G.
APPLICANT: Kumble, Krishanand D.
TITLE OF INVENTION: Compositions Isolated
TITLE OF INVENTION: and Methods for The
FILE REFERENCE: 11000.1011c2
CURRENT APPLICATION NUMBER: US/09/312,28:
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; NUMBER OF SEQ ID NO; SOFTWARE: FastSEQ I
; SEQ ID NO 262
; SEQ ID NO 262
; LENGTH: 1816
; TYPE: DMA
; ORGANISM: Mouse
US-09-312-283B-262
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            tgggagctttttacaaaggctatgttcccaatttattaggtatcataccttatgcaggca
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Pred. No. 2.2e-102;
0; Mismatches 436;
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APPLICANT: Wattson, James D.
APPLICANT: Strachan, Lorna
APPLICANT: Steeman, Matthew
APPLICANT: Sleeman, Matthew
APPLICANT: Contust, Rene
APPLICANT: Munison, James G.
APPLICANT: Kumble, Krishanand D.
TITLE OF INVENTION: Compositions Isolated Front TITLE OF INVENTION: and Methods for Their Ustrick Current APPLICATION UNMBER: US/10/152,661
CURRENT FILING DATE: 2002-05-20
PRIOR APPLICATION NUMBER: 60/221,232
PRIOR APPLICATION NUMBER: 60/221,232
PRIOR FILING DATE: 2000-07-25
PRIOR FILING DATE: 2000-05-24
PRIOR FILING DATE: 2000-05-24
PRIOR FILING DATE: 1909-05-14
PRIOR APPLICATION NUMBER: 60/312,283
PRIOR APPLICATION NUMBER: 09/312,283
PRIOR FILING DATE: 1999-04-29
PRIOR FILING DATE: 1999-04-29
PRIOR APPLICATION NUMBER: 09/312,283
PRIOR FILING DATE: 1999-04-29
PRIOR APPLICATION NUMBER: 09/312,283
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TITLE OF INVENTION: Secreted and Tra
TITLE OF INVENTION: Acids Encoding
FILE REFERENCE: P2730P1C48
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CURRENT FILING DATE: 2001-11-16
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Godowski, Paul J.
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Roy, Margaret Ann
Stewart, Timothy A.
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RESULT 12 US-10-063-502-57 Sequence 57, Application GENERAL INFORMATION: APPLICANT:
APPLICANT: APPLICANT: Eaton, Dan L. Filvaroff, Ellen Goddard, Audrey Godowski, Paul Gerritsen, Mary US/10063502 Ħ

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Matches 806; Conservative
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NUMBER OF SEQ ID NOS: 170
SEQ ID NO 57
LENGTH: 3334
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NUMBER OF SEQ ID NOS: 170
SEQ ID NO 57
LENGTH: 3334
                                                                                                                               Matches
                                                                                                                                            Query Match
Best Local Similarity
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APPLICANT: Filvaroff, E
APPLICANT: Gerritsen, N
                                                                                                                                                                                                                                                                                                                  FILE REFERENCE: P3230R1C1
CURRENT APPLICATION NUMBER: US/10/063,510
CURRENT FILING DATE: 2002-05-01
                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Watanabe, Colin K.

APPLICANT: Wood, William I.

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND TITLE OF INVENTION: ACIDS ENCODING THE SAME
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; TYPE: DNA
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APPLICANT: Wood, William I.

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: SECRETED AND THE SAME

FILE REFERENCE: P2330R1C1

CURRENT APPLICATION NUMBER: US/10/063,512

CURRENT FILING DATE: 2002-05-01

Prior Application removed - See File Wrapper or Palm

NUMBER OF SEQ ID NOS: 170

SEQ ID NO 57

LENGTH: 3334
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RESULT 15

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US-10-063-513-57

Sequence 57, Ap

GENERAL INFORMA

APPLICANT: Eat

APPLICANT: Ge

APPLICANT: Ge

APPLICANT: GO

APPLICANT: GO

APPLICANT: GO
; TYPE: DNA
; ORGANISM: Homo
US-10-063-513-57
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APPLICANT: Filvaroff, Ellen
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Goddowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Watanabe, Colin K.
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SCRETED AND TRANSMEMBRA
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3230R1C1
CURRENT APPLICATION UMBER: US/10/063,513
CURRENT FILING DATE: 2002-05-01
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                                    Prior Application removed
NUMBER OF SEQ ID NOS: 170
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LENGTH: 3334
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Search completed: August 18, 2002, 09:22:57 Job time: 7561 sec

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Post-processing: Minimum Match 0%
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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85.9 410 21 US-09-777-921-5 71.8 342 21 US-09-777-921-6	95.6 475 21 US-09-777-921-4 90.5 470 1 PCT-US01-14827-10548	100.0 477 21 US-09-777-921-2 99.6 477 1 PCT-US01-04098A-1739	Result Query No. Score Match Length DB ID De
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ALIGNMENTS

RESULT

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US-09-777-921-2

Sequence 2, Application US/09777921

GENERAL INFORMATION:
APPLICANT: MERKULOV et al
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                                                                                                                                                 ; TYPE: PRT; ORGANISM: Homo sapiens PCT-US01-04098A-1739
                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: Not Yet Assigned PRIOR FILING DATE: 2001-01-30
PRIOR PRIOR PRIOR DATE: 2001-11-30
PRIOR PRIOR APPLICATION NUMBER: 09/728,422
PRIOR APPLICATION NUMBER: 09/693,325
PRIOR FILING DATE: 2000-10-20
PRIOR PRIOR PRIOR PRIOR 109/663,561
PRIOR PRIOR PRIOR DATE: 2000-09-15
PRIOR APPLICATION NUMBER: 09/663,561
PRIOR APPLICATION NUMBER: 09/654,936
PRIOR APPLICATION NUMBER: 09/620,325
PRIOR APPLICATION NUMBER: 09/620,325
PRIOR APPLICATION NUMBER: 09/598,075
PRIOR APPLICATION NUMBER: 09/598,075
PRIOR APPLICATION NUMBER: 09/560,875
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Best I
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                                                                                Matches
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                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 09/496,914
PRIOR FILING DATE: 2000-02-03
NUMBER OF SEQ ID NOS: 3960
SOFTWARE: Custom
SEQ ID NO 1739
LENGTH: 477
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides FILE REFERENCE: 21272-029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Hyseq,
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                                                                                            Local Similarity
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                        MLRWLRDFALFTAACQDAEQFTRYETLFQALDRNGDGVVDIGELQEGLRNLGIPLGQDAE
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EKIFTTGDVNKDGKLDFEEFMKYLKDHEKKMKLAFKSLDKNNDGKIEASEIVQSLQTLGL
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                                                                             99.6%;
nilarity 99.6%;
Conservative
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                                                                             Score 2471; DB 1;
Pred. No. 1.8e-213;
0; Mismatches 2;
                                                                                                      Length
                                                                                                          477;
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US-09-777-921-4
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Best Local Sim
Matches 454;
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TAQTFIYPMEVMKTRLAVGKTGQYSGIYDCAKKILKHEGLGAFYKGYVPNLLGIIPYAGI
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; LENGTH: 475
; TYPE: PRT
; ORGANISM: Rabbit
US-09-777-921-4
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CURRENT FILING DATE: 2001-07-02
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
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TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HU
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: CL001103
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                                                                                                                                                            TISEQQAELILQSIDVDGTMTVDWNEWRDYFLFNPVTDIEEIIRFWKHSTGIDIGDSLTI 180
TAQTFIYPMEVMKTRLAVGKTGQYSGIYDCAKKILKHEGLGAFYKGYVPNLLGIIPYAGI 360
                                                                                                   PDEFTEDEKKSGOWWROLLAGGIAGAVSRTSTAPLDRLKIMMQVHGSKSDKMNIFGGFRQ 240
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                                                                              EKIFTTGDVNKDGKLDFEEFMKYLKDHEKKMKLAFKSLDKNNDGKIEASEIVQSLQTLGL 120
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95.2%;
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Pred. No. 1.3e-204;
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OTHER INFORMATION: MITOCHONDRIAL CARRIER PROTEIN SIGNATURE domain identified
OTHER INFORMATION: eMATRIX, accession number PR00926F, p-value=7.750e-19, raw
OTHER INFORMATION: 17.75
NAME/KEY: DOMAIN
LOCATION: (222)..(466)
OTHER INFORMATION: Mitochondrial carrier proteins domain identified by PFam,
OTHER INFORMATION: accession name mito_carr, E-value=7.2e-71, PFam score of 2
PCT-US01-14827-10548
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PCT-US01-14827-10548
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Best Local Sim
Matches 436;
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SOFTWARE: Custom
SEQ ID NO 10548
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TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND
FILE REFERENCE: 21272-104
CURRENT APPLICATION NUMBER: PCT/US01/14827
CURRENT FILING DATE: 2001-05-16
PRIOR APPLICATION NUMBER: 09/577,408
PRIOR FILING DATE: 2000-05-18
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NAME/KEY: DOMAIN
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               DLAVYELLKSYWLDNFAKDSVNPGVMVLLGCGALSSTCGQLASYPLALVRTRMQAQAMLE
                                                        MVKEGGIRSLWRGNGTNVIKIAPETAVKFWAYEQYKKLLTEEGQKIGTFERFISGSMAGA
                                                                                                                                                                           EKIFTTGDVNKDGKLDFEEFMKYLKDHEKKMKLAFKSLDKNNDGKIEASEIVQSLQTLGL 120
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DLAVYELLKSYWLDNFAKDSVNPGVMVLLGCGALSSTCGQLASYPLALVRTRMQAQAMLE
                                                                                                                   MVKEGGIRSLWRGNGTNVIKIAPETAVKFWAYEQ-------
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                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                     90.5%; Score 2246; DB 1;
91.4%; Pred. No. 3.6e-193;
tive 2; Mismatches 3;
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Sequence 6, Application US/09777921

GENERAL INFORMATION:
APPLICANT: MERKULOV et al
ITILE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
ITILE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN
ITILE OF INVENTION: AND USES THEREOF
FILE REFERENCE: CL001103

CURRENT APPLICATION NUMBER: US/09/777,921

CURRENT FILING DATE: 2001-07-02

NUMBER OF SEQ ID NOS: 6

SOFTWARE: FastSEQ for Windows Version 4.0

LENGTH: 342
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US-09-777-921-5
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; Sequence 5, Application US/09777921
; GENERAL INFORMATION:
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SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 5
LENGTH: 410
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Best Local Similarity
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CURRENT APPLICATION NUMBER: US/09/777,921

CURRENT FILING DATE: 2001-07-02
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HUMAN TRANSPORTER

PROTEINS

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; ORGANISM: Human
US-09-777-921-6
                                                                                                                                                                                                                                             ; ORGANISM: Human PCT-US01-21148-6
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PCT-US01-21148-6
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Best Local S
Matches 300
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SOFTWARE: FastSEQ for
SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 60/216,340
PRIOR FILING DATE: 2000-07-05
PRIOR APPLICATION NUMBER: 09/810,673
PRIOR APPLICATION NUMBER: 09/810,673
PRIOR FILING DATE: 2001-03-19
NUMBER OF SEC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 6, Application PC/TUS0121148 GENERAL INFORMATION:
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Best Local
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TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUM
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: CL0007239CT
CURRENT APPLICATION NUMBER: PCT/US01/21148
CURRENT FILING DATE: 2001-07-03
                                                                                                                                                                                                                                                                        TYPE: PRT
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  121
                               137
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les 300; Conserv
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nes 342; Conserv
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  DGTMTVDWNEWRDYFLFNPVTDIEEIIRFWKHSTGIDIGDSLTIPDEFTEDEKKSGQWWR
              DGTMTVDWNEWRDYfLFNPVTDIEEIIRFWKHSTGIDIGDSLTIPDEFTEDEKKSGQWWR 196
                                                                     FEEFMKYLKDHEKKMKLAFKSLDKNNDGKIEASEIVQSLQTLGLTISEQQAELILQSIDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YDCAKKILKHEGLGAFYKGYVPNLLGIIPYAGIDLAVYELLK 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FQALDRNGDGVVDIGELQEGLRNLGIPLGQDAEEKIFTTGDVNKDGKLDFEEFMKYLKDH 87
                                                        FEEFMKYLKDHEKKMKLAFKSLDKNNDGKIEASEIVQSLQTLGLTISEQQAELILQSIDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SRTSTAPLDRLKIMMQVHGSKSDKMNIFGGFRQMVKEGGIRSLWRGNGTNVIKIAPETAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EKKMKLAFKSLDKNNDGKIEASEIVQSLQTLGLTISEQQAELILQSIDVDGTMTVDWNEW 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SRTSTAPLDRLKIMMQVHGSKSDKMNIFGGFRQMVKEGGIRSLWRGNGTNVIKIAPETAV
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                                                                                                                                                                        0;
                                                                                                                                                                                   Score 1560; DB 1;
Pred. No. 1.3e-131;
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; LENGTH: 300
; TYPE: PRT
; ORGANISM: Human
US-09-810-673A-6
CURRENT APPLICATION NUMBER: PCT/US01/04926A
CURRENT FILING DATE: 2001-02-26
PRIOR APPLICATION NUMBER: 09/664,641
PRIOR FILING DATE: 2000-09-19
PRIOR APPLICATION NUMBER: 09/616,807
PRIOR FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: 09/597,707
PRIOR APPLICATION NUMBER: 09/597,707
PRIOR FILING DATE: 2000-05-18
PRIOR APPLICATION NUMBER: 09/577,409
PRIOR APPLICATION NUMBER: 09/517,409
PRIOR APPLICATION NUMBER: 09/515,126
                                                                                                                                                                                                                                                                           RESULT 9
PCT-US01-04926A-194
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US-09-810-673A-6
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                                                                                                                                                                                                                                           Sequence 194, Application PC/TUS0104926A GENERAL INFORMATION:
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Best Local Similarity
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TITLE OF INVENTION: INSCLATED HOLECULES ENCODING HUMAN TRANSPORTER PROTEINS
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: CL000723
                                                                                                                                                                                           TITLE OF INVENTION: Novel Nucleic Acids and FILE REFERENCE: 21272-041
                                                                                                                                                                                                                             APPLICANT: Hyseq,
                                                                                                                                                                                                                                                                                                                                                                                     257
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                                                                                                                                                                                                                                                                                                                                               241 NVIKIAPETAVKFWAYEQYKKLLTEEGQKIGTFERFISGSMAGATAQTFIYPMEVMKTRL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEEFMKYLKDHEKKMKLAFKSLDKNNDGKIEASEIVQSLQTLGLTISEQQAELILQSIDV 136
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                                                                                                                                                                                                                             Inc.
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 Mismatches

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TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
FILE REFERENCE: 21272-041
CURRENT APPLICATION NUMBER: PCT/US01/04926A
CURRENT FILING DATE: 2001-02-26
PRIOR APPLICATION NUMBER: 09/664,641
PRIOR FILING DATE: 2000-09-19
PRIOR APPLICATION NUMBER: 09/616,807
PRIOR FILING DATE: 2000-07-14
PRIOR FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: 09/597,707
PRIOR APPLICATION NUMBER: 09/597,707
PRIOR APPLICATION NUMBER: 09/597,409
PRIOR APPLICATION NUMBER: 09/577,409
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PCT-US01-04926A-538
                                                                                                                                                                                                                                                                                                                                                                                                          PCT-US01-04926A-538
                            NUMBER OF SEQ ID ISOFTWARE: Custom SEQ ID NO 538
LENGTH: 509
TYPE: PRT
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LENGTH: 471
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Best Local Similarity
                                                                                                                 PRIOR APPLICATION NUMBER: 09/515,126 PRIOR FILING DATE: 2000-02-28
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SOFTWARE: Custom
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               ORGANISM: Homo
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DAERRQRWGRLFEELDSNKDGRVDVHELRQGLARLG---GGNPDPGAQQGISSEGDADPD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HILSQEGMRGLYRGIAPNFMKVIPAVSISYVVYENMKQALGVTSR
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61.5%;
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Pred. No. 1.3e-130;
5; Mismatches 87;
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                                                                                                                                  PRIOR APPLICATION NUMBER: PCT/US99/1252
PRIOR FILING DATE: 1999-06-02
PRIOR APPLICATION NUMBER: US 60/087,607
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: US 60/087,609
PRIOR APPLICATION NUMBER: US 60/087,759
PRIOR APPLICATION NUMBER: US 60/087,759
PRIOR FILING DATE: 1998-06-03
PRIOR PRIOR DATE: 1998-06-03
PRIOR APPLICATION NUMBER: US 60/087,827
PRIOR FILING DATE: 1998-06-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Baker, K.
APPLICANT: Chen, Ji.
APPLICANT: Goddard,
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Best Local S
Matches 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 289,
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CURRENT APPLICATION NUMBER: US/09/709,238
CURRENT FILING DATE: 2000-11-08
                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Wood, W
APPLICANT: Yuan, J.
TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               193 QWWRQLLAGGIAGAVSRTSTAPLDRLKIMMQVHGSKSDKMNIFGGFRQMVKEGGIRSLWR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              222 MWWKQLVAGAVAGAVSRTGTAPLDRLKVFMQVHASKTNRLNILGGLRSMVLEGGIRSLWR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  102 GGLDLEEFSRYLQEREQRLLLMFHSLDRNQDGHIDVSEIQQSFRALGISISLEQAEKILH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       45 DAERRORWGRLFEELDSNKDGRVDVHELROGLARLG---GGNPDPGAQQGISSEGDADPD 101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 61.9 cs 286; Conservative
FILING DATE: 1998-06-04
APPLICATION NUMBER: US 60/088,028
FILING DATE: 1998-06-04
APPLICATION NUMBER: US 60/088,029
FILING DATE: 1998-06-04
                                                                                 APPLICATION NUMBER: US FILING DATE: 1998-06-04 APPLICATION NUMBER: US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KTRLTLRRTGQYKGLLDCARRILEREGPRAFYRGYLPNVLGIIPYAGIDLAVYETLKNWW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GNGINVLKIAPESAIKFMAYEQIKRAILGQQETLHVQERFVAGSLAGATAQTIIYPMEVL
                                                                                                                                                                                                                                                                                                                                                                               Gurney, Austin
Smith, Victoria
Watanabe, Colin K
Wood, William I.
Yuan, Jean
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chen, Jian
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Baker, Kevin
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                                                                                    60/088,025
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Pred. No. 1.5e-130;
5; Mismatches 87;
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R FILING DATE: 1998-01
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1998-06-10

NUMBER: US 6: 1998-06-10

60/088,826

APPLICATION NUMBER: US 60/088,858
FILING DATE: 1998-06-11
APPLICATION NUMBER: US 60/088,861
FILING DATE: 1998-06-11

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1998-06-11 MBER: US 60/088,876

US 60/088,863

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60/088,810

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1998-06-10 NUMBER: US 60/088,811 1998-06-10 NUMBER: US 60/088,824

1998-06-10 UMBER: US 60/088,825

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OR APPLICATION NUMBER: US 60/088,730
OR FILING DATE: 1998-06-10
OR APPLICATION NUMBER: US 60/088,734
OR FILING DATE: 1998-06-10
OR APPLICATION NUMBER: US 60/088,738
OR APPLICATION NUMBER: US 60/088,738
OR APPLICATION NUMBER: US 60/088,736
OR APPLICATION NUMBER: US 60/088,740
OR FILING DATE: 1998-06-10

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OR FILING DATE: 1988-06-05
OR APPLICATION NUMBER: US 60/088,202
OR FILING DATE: 1998-06-05
OR FILING DATE: 1998-06-05
OR APPLICATION NUMBER: US 60/088,212
OR FILING DATE: 1998-06-05
OR APPLICATION NUMBER: US 60/088,655
OR APPLICATION NUMBER: US 60/088,655
OR APPLICATION NUMBER: US 60/088,722
OR FILING DATE: 1998-06-10

US 60/088, 202

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NUMBER: US : 1998-06-04

60/088,030

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APPLICATION FILING DATE:

NUMBER: US 60/089,514: 1998-06-16

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лььк: US 60/089,599 1998-06-17 Мырро

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NUMBER: US 60/089,801: 1998-06-18 NUMBER: US 60/089,653 NUMBER: US 60/089,600: 1998-06-17

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OR APPLICATION NUMBER: US 60/089,090
OR FILING DATE: 1998-06-12
OR APPLICATION NUMBER: US 60/089,105
OR FILING DATE: 1998-06-12
OR APPLICATION NUMBER: US 60/089,440
OR FILING DATE: 1998-06-16
OR APPLICATION NUMBER: US 60/089,512
OR FILING DATE: 1998-06-16

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Sequence 289
GENERAL INFO
APPLICANT:
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IOR FILING DATE: 1998-07-02
IOR APPLICATION NUMBER: US 60/091,628
IOR APPLICATION NUMBER: US 60/091,633
IOR APPLICATION NUMBER: US 60/091,633
IOR APPLICATION NUMBER: US 60/091,633
IOR FILING DATE: 1998-07-02
IOR APPLICATION NUMBER: US 60/091,673
IOR FILING DATE: 1998-07-02
IOR APPLICATION NUMBER: US 60/091,978
IOR APPLICATION NUMBER: US 60/091,978
IOR FILING DATE: 1998-07-07
IOR APPLICATION NUMBER: US 60/091,982
IOR FILING DATE: 1998-07-07
IOR APPLICATION NUMBER: US 60/092,182
IOR FILING DATE: 1998-07-09
IOR APPLICATION NUMBER: US 60/092,182
IOR FILING DATE: 1998-07-09
IOR APPLICATION NUMBER: US 60/092,182
IOR FILING DATE: 1998-07-09
IOR APPLICATION NUMBER: US 60/092,472
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                                                                                                                                                                                e 289, Application US/09941992 INFORMATION:
                                                                                                                                                                                                                                                                     ATAQTEIYPMEVMKTRLAVGKTGQYSGIYDCAKKILKHEGLGAFYKGYVPNLLGIIPYAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QMVKEGGIRSLWRGNGTNVIKIAPETAVKFWAYEQYKKLLTEEGQKIGTFERFISGSMAG
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                                                                                     Botstein, David
Desnoyers, Luc
Eaton, Dan L.
Ferrara, Napoleone
                                                                                                                                                                Ashkenazi, Avi J.
Gerritsen, Mary E.
Goddard, Audrey
Godowski, Paul J.
Grimaldi, J.Christopher
                                                                          Fong,
                                                           Gerber, Hanspeter
                                                                                                                                                  Baker, Kevin P
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                                                                           Sherman
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65.8%;
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Pred.
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Mismatches
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No. 5
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5.8e-126;
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PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR APPLICATION NUMBER: 60/065311
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR FILING DATE: 1997-11-13
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                                          PRIOR
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                                              KQKIVQAGDKDLDGQLDFEEFVHYLQDHEKKLRLVFKILDKKNDGRIDAQEIMQSLRDLG
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TITLE OF INVENTION: Secreted and Transmembrane
TITLE OF INVENTION: Secreted and Transmembrane
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730p1C56
CURRENT APPLICATION NUMBER: US/09/989,279
CURRENT APPLICATION NUMBER: 00/049787
PRIOR APPLICATION NUMBER: 60/049787
PRIOR APPLICATION NUMBER: 60/049787
PRIOR APPLICATION NUMBER: 60/049787
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PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR FILING DATE: 1997-11-12
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OR APPLICATION NUMBER: 60/087106
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OR APPLICATION NUMBER: 60/087609
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APPLICATION NUMBER: 60/078910
FILING DATE: 1998-03-20
APPLICATION NUMBER: 60/083322
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FILING DATE: 1998-06-03
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FILING DATE: 1998-02-25
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APPLICATION NUMBER: 60/065311
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Roy, Margaret Ann
Stewart, Timothy /
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Kljavin,Ivar J.
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Godowski, Paul J.
Grimaldi, J.Christopher
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Desnoyers, Luc
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Pred. No. 5.8e-126;
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RESULT 14
US-09-989-293A-289
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PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR FILING DATE: 1997-06-17
PRIOR FILING DATE: 1997-10-17
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR APPLICATION NUMBER: 60/065116
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
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TITLE OF INVENTION: Secrete
TITLE OF INVENTION: Acids
FILE REFERENCE: P2730P1C66
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APPLICANT: Geritten, Mary E.
APPLICANT: Goddard, Andrey
APPLICANT: Goddwski, Paul J.
APPLICANT: Goddwski, Paul J.
APPLICANT: Grimaldi, J.Christopher
APPLICANT: Grimaldi, J.Christopher
APPLICANT: Kljavin, Ivar J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Paon, James
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Abnoy, Zemin
TITLE OF INVENTION: Secreted and Transmembra
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730PlC55
CURRENT APPLICATION NUMBER: 60/049787
PRIOR APPLICATION NUMBER: 60/049787
PRIOR APPLICATION NUMBER: 60/062250
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PR APPLICATION NUMBER: 60/091633

PR FILING DATE: 1998-07-02

PR APPLICATION NUMBER: 60/091978

PR FILING DATE: 1998-07-07

PR APPLICATION NUMBER: 60/091982
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FILING DATE: 1998-07-02
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DR FILING DATE: 1998-07-02
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EGAPEVIMSSLFKHILRTEGAFGLYRGLAPNFMKVIPAVSISYVVYENLKITLGVQSR
              EGSPQLNMVGLFRRIISKEGIPGLYRGITPNFMKVLPAVGISYVVYENMKQTLGVTQK
                                           IPDEFTEDEKKSGQWWRQLLAGGIAGAVSRTSTAPLDRLKIMMQVHGSKSDKMNIFGGFR
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Search completed: Job time: 657 sec August 18, 2002, 09:27:03

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2: /cgn2_6/ptodata/1/paa/US06_NEW_COMB.pep:*

3: /cgn2_6/ptodata/1/paa/US07_NEW_COMB.pep:*

4: /cgn2_6/ptodata/1/paa/US08_NEW_COMB.pep:*

5: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:*

6: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:*

7: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:*
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; Sequence 130652, Application U;
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIM
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TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUM
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: CL001103
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SOFTWARE: FastSEQ for Windows Version
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FILE REFERENCE: 261/210

CURRENT APPLICATION NUMBER: US/09/791,537

CURRENT FILING DATE: 2001-02-22

NUMBER OF SEQ ID NOS: 153055

SOFTWARE: Patentin version 3.0

SEQ ID NO 130652

LENGTH A75
                                                                                                                                                                  Sequence 5, Application US/09777921A

GENERAL INFORMATION:

APPLICANT: MERKULOV et al.

TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,

TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN

TITLE OF INVENTION: AND USES THEREOF

FILE REFERENCE: CL001103

CURRENT APPLICATION NUMBER: US/09/777,921A

CURRENT APPLICATION NUMBER: US/09/777,921A

CURRENT FILING DATE: 2002-02-07

NUMBER OF SEQ ID NOS: 126

SOFTMARE: FastSEQ for Windows Version 4.0
                                                                                  ; TYPE: PRT
; ORGANISM: Homo
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                                                                                                                                                       SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
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TYPE: PRT
                                                                                                                                     LENGTH: 410
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                  85.9%;
99.8%;
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Score 2132; DB 5;
Pred. No. 2.5e-166;
D; Mismatches 1;
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Query Match Best Local S Matches 409

al Similarity 409; Conser

Conservative

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Length 410;

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300

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APPLICANT: Bionomix, Inc.

APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
APPLICANT: Debe, Toseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF
TITLE OF INVENTION: METHODS OF USE THEREOF
FILLE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT APPLICATION STRUCTURE 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
SEQ ID NO 131726
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US-09-791-537-131726
Sequence 131726, Application
GENERAL INFORMATION:
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Best Local Similarity
Matches 409; Conser
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                RSLWRGNGTNVIKIAPETAVKFWAYEQYKKLLTEEGQKIGTFERFISGSMAGATAQTFIY
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                                          EKKSGQWWRQLLAGGIAGAVSRTSTAPLDRLKIMMQVHGSKSDKMNIFGGFRQMVKEGGI
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411
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                                                                                                                                                                                                                                                                  85.9%; Score 2132; I
99.8%; Pred. No. 2.50
tive 0; Mismatches
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                                                                                                                                                                                                                                                                                DB 5;
2.5e-166;
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RESULT 7
US-09-777-921A-6
; Sequence 6, Application
; GENERAL INFORMATION:
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APPLICANT: Warnock, Dale E.
TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
FILE REFERENCE: 660088.465P2
CURRENT APPLICATION NUMBER: US/60/389,987
CURRENT FILING DATE: 2002-06-17
NUMBER OF SEQ ID NOS: 3025
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 765
LENGTH: 411
TYPE: Dam
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Best Local Similarity
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                                                                                                                                         PMEVMKTRLAVGKTGQYSGIYDCAKKILKHEGLGAFYKGYVPNLLGIIPYAGIDLAVYEL
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Taylor, Steven W.
Glenn, Gary M.
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              US/09777921A
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    Mismatches

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Length Indels

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Gaps

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RESULT 8
US-09-991-150-289
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NUMBER OF SEQ ID NOS: 126
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6
LENGTH: 342
                                                                                                                                                                                                                                                                                                                              Sequence 289, Application GENERAL INFORMATION:
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Best Local Similarity 100.0%;
Matches 342; Conservative
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APPLICANT:
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APPLICANT:
APPLICANT:
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APPLICANT:
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TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUM
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: CLOOI103
CURRENT APPLICATION NUMBER: US/09/777,921A
CURRENT FILING DATE: 2002-02-07
                                                                                    APPLICANT: APPLICANT:
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                                APPLICANT:
                                             APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                YDCAKKILKHEGLGAFYKGYVPNLLGIIPYAGIDLAVYELLK 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KFWAYEQYKKLLTEEGQKIGTFERFISGSMAGATAQTFIYPMEVMKTRLAVGKTGQYSGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EKKMKLAFKSLDKNNDGKIEASEIVQSLQTLGLTISEQQAELILQSIDVDGTMTVDWNEW 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FQALDRNGDGVVDIGELQEGLRNLGIPLGQDAEEKIFTTGDVNKDGKLDFEEFMKYLKDH
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                                                                                                                                                     Gerber, Hanspeter
Gerritsen, Mary E.
Goddard, Audrey
Godowski, Paul J.
Grimaldi, J. Christopher
                                                                                                                                                                                                                                                                                                                Ashkenazi, Avi J.
Watanabe, Colin K. Williams, P. Mickey Wood, William I.
                                                     Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
                                             Tumas,
                                                                                                                                         Gurney, Austin L.
                                                                                                                                                                                                                               Fong, Sherman
                                                                                                                                                                                                                                                                                                   Baker, Kevin P
                                                                                                   Pan, James
                                                                                                             Napier, Mary A.
                                                                                                                            Kljavin, Ivar J.
                                                                                                                                                                                                                                         Ferrara, Napoleone
                                                                                                                                                                                                                                                         Eaton, Dan L.
                                                                                                                                                                                                                                                                       Desnoyers, Luc
                                                                                                                                                                                                                                                                                      Botstein, David
                                         Daniel
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US-10-063-502-58
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                                               Prior Application removed
NUMBER OF SEQ ID NOS: 170
SEQ ID NO 58
LENGTH: 469
                                                                                                                                                                                                                                                                                                                             Sequence 58, Application US/10063502
GENERAL INFORMATION:
APPLICANT: Eaton, Dan L.
APPLICANT: Filvaroff, Ellen
                                                                                                                                                                                                                                         APPLICANT: APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 289
                                                                                                                                                                                                                                                                                          APPLICANT:
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Secreted and Transmembrane Polypeptides TITLE OF INVENTION: Acids Encoding the Same EILE REFERENCE: pz730p1c48

CURRENT APPLICATION NUMBER: US/09/991,150

CURRENT FILING DATE: 2001-11-16

Prior Application removed - See File Wrapper or Palm NUMBER OF SEQ ID NOS: 532
                                                                                                                                                      TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3230R1C1
                                                                                                                    CURRENT APPLICATION NUMBER: US/10/063,502 CURRENT FILING DATE: 2002-05-01
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TYPE: PRT
ORGANISM: Homo sapiens
                                  TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EEKIFTTGDVNKDGKLDFEEFMKYLKDHEKKMKLAFKSLDKNNDGKIEASEIVQSLQTLG 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EGAPEVTMSSLFKHILRTEGAFGLYRGLAPNFMKVIPAVSISYVVYENLKITLGVQSR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATAQTEIYPMEVMKTRLAVGKTGQYSGIYDCAKKILKHEGLGAFYKGYVPNLLGIIPYAG 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VPDEFTVEERQTGMWWRHLVAGGGAGAVSRTCTAPLDRLKVLMQVHASRSNNMGIVGGFT 231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IDLAVYETLKNAWLQHYAVNSADPGVFVLLACGTMSSTCGQLASYPLALVRTRMQAQASI 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QMIREGGARSLWRGNGINVLKIAPESAIKFMAYEQIKRLVGSDQETLRIHERLVAGSLAG
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              Homo Sapier
                                                                                                                                                                                                         Watanabe, Colin Wood, William I.
                                                                                                                                                                                                                                           Grimaldi, Christopher Gurney, Austin L.
                                                                                                                                                                                                                                                                              Godowski, Paul J.
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                                                                                                   See
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Length 469;

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                                                                                                                          Query Match
Best Local S
Matches 275
                                                                                                                                                                                                                                                                    Prior Application removed - NUMBER OF SEQ ID NOS: 170 SEQ ID NO 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 58, Application US/10063510 GENERAL INFORMATION:
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Best Local Similarity
Matches 275; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                APPLICANT: Watanabe, Colin K.
APPLICANT: WOOG, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3230R1C1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Eaton, Dan L. APPLICANT: Filvaroff, E APPLICANT: Gerritsen, M
                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/10/063,510 CURRENT FILING DATE: 2002-05-01
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   112
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::|| || :||:|||||: ||:|||||: ||
KQKIVQAGDKDLDGQLDFEEFVHYLQDHEKKLRLVFKILDKKNDGRIDAQEIMQSLRDLG 111
                  LTISEQQAELILQSIDVDGTMTVDWNEWRDYFLFNPVTDIEEIIRFWKHSTGIDIGDSLT 179
                                                             KQKIVQAGDKDLDGQLDFEEFVHYLQDHEKKLRLVFKILDKKNDGRIDAQEIMQSLRDLG
                                                                             EEKIFTTGDVNKDGKLDFEEFMKYLKDHEKKMKLAFKSLDKNNDGKIEASEIVQSLQTLG 119
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VKISEQQAEKILKSMDKNGTMTIDWNEWRDYHLLHPVENIPEIILYWKHSTIFDVGENLT
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Godowski, Paul J.
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                                                                                                                        60.5%; Score 1501; [65.8%; Pred. No. 1.56
tive 71; Mismatches
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                                                                                                                                                                                                                                                                                                   See File Wrapper or
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                                                                                                                          l.5e-114;
nes 72;
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                                                                                                                                                        Length 469;
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRA
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3230R1C1
CURRENT APPLICATION NUMBER: US/10/063,512
CURRENT FILING DATE: 2002-05-01
Prior Application removed - See File Wrapper
NUMBER OF SEQ ID NOS: 170
SEQ ID NO 58
LENGTH: 469
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                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
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ATAQTETYPMEVMKTRLAVGKTGQYSGTYDCAKKILKHEGLGAFYKGYVPNLLGTIPYAG
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Grimaldi, Christopher
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                                                                                                                                                                                                                                                                       60.5%; Score 1501; DB 6; 65.8%; Pred. No. 1.5e-114; tive 71; Mismatches 72;
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; ORGANISM: Homo Sapien
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US-10-063-513-58
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APPLICANT: Filvaroff, El
APPLICANT: Gerritsen, Ma
APPLICANT: Goddard, Audr
APPLICANT: Goddwski, Pau
APPLICANT: Goddwski, Pau
Sequence 58, Application US/10063514
GENERAL INFORMATION:
APPLICANT: Eaton, Dan L.
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Best Local Similarity
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LENGTH: 469
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                                                                                                                                                                                                     QMVKEGGIRSLWRGNGTNVIKIAPETAVKFWAYEQYKKLLTEEGQKIGTFERFISGSMAG 299
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                                                                                              EGAPEVTMSSLFKHILRTEGAFGLYRGLAPNFMKVIPAVSISYVVYENLKITLGVQSR
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Grimaldi, Christopher J
Gurney, Austin L.
Watanabe, Colin K.
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US-10-063-515-58
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                                                                Grimaldi,Christopher J.
Gurney,Austin L.
Watanabe,Colin K.
Wood,William I.
                                                                                                                                   Gerritsen, Mary
Goddard, Audrey
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Gerritsen, Mary
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3230R1C1 CURRENT APPLICATION NUMBER: US/10/063,515 CURRENT FILING DATE: 2002-05-01
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CURRENT FILING DATE: 2002-05-01
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Pred. No. 1.5e-114;
71; Mismatches 72;
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                                                                                                                                                                                                                                                                                                      Sequence 58, Application US/10063516 GENERAL INFORMATION: APPLICANT: Eaton, Dan L.
            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                     APPLICANT:
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                                                                                                           SEQ ID NO 58
   Matches 275;
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                                                                                                                   APPLICANT: WOOD, WILLIAM I.

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3230R1C1
CURRENT APPLICATION NUMBER: US/10/063,516
CURRENT FILING DATE: 2002-05-01
PTIOT APPLICATION TEMOVED - See File Wrapper of
NUMBER OF SEQ ID NOS: 170
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                                                                                   LENGTH: 469
TYPE: PRT
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Godowski, Paul J.
Grimaldi, Christopher J.
Gurney, Austin L.
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60.5%; Score 1501; DB 6; 65.8%; Pred. No. 1.5e-114; tive 71; Mismatches 72;
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Search completed: August 18, 2002, 09:28:54 Job time: 474 sec

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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ALIGNMENTS

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VERSION JOURNAL REFERENCE AUTHORS TITLE REFERENCE AUTHORS TITLE KEYWORDS SOURCE ORGANISM RESULT AF123303 FEATURES JOURNAL source 2 (bases 1 to 3259)
Biery, B. and Valle, D.
Direct Submission
Submitted (25-JAN-1999) Pediatrics/Genetics, Johns Hopkins
University, 725 N. Wolfe Street PCTB 803, Baltimore, MD 21205, USA
1. .3259 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 3259)
Biery, B. and Valle, D. Cloning and subcellular localization of a human calcium-binding 3259
Homo sapiens calcium-binding
AF123303
AF123303.1 GI:6841065 Unpublished transporter Homo sapiens human. עי מאוא linear PRI 01-FEB-2000 transporter mRNA, partial cds. Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.

Result No.

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                                            Direct Submission
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Universitaetsspital, Raemistr. 100,
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                                                                                                                                                                                                                           AAGTCTACTTTTTTTTTTTTCCCACCAGGGGAAGAACATATCAACAATCACTTCAAA
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E 2 (bases 1 to 170026)

S Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M.,
Baldwin,J., Barna,N., Beckerly,R., Boguslavkiy,L., Boukhgalter,B.,
Brown,A., Castle,A., Colangelo,M., Collins,S., Collymore,A.,
Cooke,P., DeArellano,K., Dewar,K., Domino,M., Donelan,L., Doyle,M.,
Ferreira,P., FitzHugh,W., Forrest,C., Funke,R., Gage,D.,
Galagan,J., Gardyna,S., Grant,G., Hagos,B., Heaford,A., Horton,L.,
Galagan,J., Gardyna,S., Grant,G., Rann,L., Karatas,A., Klein,J.,
Howland,J.C., Johnson,R., Jones,C., Kann,L., Karatas,A., Klein,J.,
Lehoczky,J., Lieu,C., Locke,K., Macdonald,P., Marquis,N.,
McGrewan,P., McGurk,A., McKernan,K., McLaughlin,J., Meldrim,J.,
Morrow,J., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,
Peterson,K., Pollara,V., Riley,R., Roy,A., Santos,R., Severy,P.,
Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,
Tesfaye,S., Tirrell,A., Vassiliev,H., Vo,A., Wheeler,J., Wu,X.,
Wyman,D., Ye,W.J., Zimmer,A. and Zody,M.
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                                                                                                                                         http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
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Unpublished
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Birren, B., Linton, L.,
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Center
Center
                                                           Contact: sequence_submissions@genome
                                                                              Web site: http://www-seq.wi.mit.edu
                                                                                                 Center code: WIBR
                                                                                                                         Center: Whitehead Institute/ MIT
project name: L3222 clone name: 11_L_4
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clone RP11-11L4,
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                            tgactttttctcctcgaattgaaacaagtctatggcaaaagaagctgcatttttttcaca 1684
TGACTTTTTCTCCTCGAATTGAAACAAGTCTATGGCAAAAGAAGCTGCATTTTTTTCACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
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119119 119218: gap of 100 bp
119219 170026: contig of 50808 bp
Location/Qualifiers
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Insert size: 169726; sum-of-contigs
Quality coverage: 5.3 in Q20 bases; agarose-fp
Quality coverage: 5.4 in Q20 bases; sum-of-contigs
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119219. .170026
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70801. .119118
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/db_xref="taxon:9606"
/clone="RP11-11L4"
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34183 c 34647 g 50780
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98.7%;
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SOURCE

ORGANISM

Homo sapiens Eukaryota; Metazoa; Mammalia; Eutheria;

Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo.

KEYWORDS

HTG. AL390036 AL390036.17

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JOURNAL
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 1167;
                                                                                                                                                                                                                                                                                                      151015 AGCCATGTTAGAAGGTTCCCCACAGCTGAATATGGTTGGCCTCTTTCGACGAATTATTTC 150956
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gaaatgatgttgcattttttgctttagcctgataattgaaactttcaacaatctctggag 1624
                                                              TGCTGTAGGCATCAGTTATGTGGTTTATGAAAATATGAAGCAAACTTTAGGAGTAACCCA
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This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one Mi3 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers give in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr., TREMBL; Wp:, WORMPEP; Information on the WORMPEP
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On Sep 7, 2001 this sequence version replaced gi:14456226.
During sequence assembly data is compared from overlapping clones
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RP11-356N1 is from the library RPCI-11.2 constructed of Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm
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48723. .49036
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(AL391235). Assembly confirmed by restriction dig
79012. .79019
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98.6%;
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Pred. No. 1.6e-202;
0; Mismatches 14;
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RESULT AL356110 LOCUS

DEFINITION

Homo sapiens chromosome sequencing in PROGRESS :

IN PROGRESS ***,

159384 bp DNA linear HTG 15-MAY-2000 ne 1 clone RP4-562N20 map p34.1-34.2, *** ; ***, 71 unordered pieces.

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JOURNAL
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Quality coverage: 1.75x in Q20 bases;
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----- Project Informa
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On Jul 15, 2000 this sequence version replaced gi:7899229.
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1 (bases 1 to 159384)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         NOTE: This is a 'working draft' sequence. It currently consists of 71 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as
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                                                     851;
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Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human
Center, Stanford University School of Medicine, Stanford,
Web site: http://www-shgc.stanford.edu
Contact: (Dickson, Mark) mod@paxil.stanford.edu
Contact: (Dickson, Mark) mod@paxil.stanford.edu
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Contact: MGC help desk
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Direct Submission
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nmalia; Eutheria; Rodentia;
(bases 1 to 1089)
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                                                                                                                                                                                                                                                                                                       293
                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                    /protein_id="unknown (protein for IMAGE:4208509)"
/protein_id="AAH22837.1"
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IPNLLGIIPYAGIDLAVYELLKSYMLDNEAKDSVNPGVMVLLSCGALSSTCGQLASYP
LALVRTRWQAQATVEGAPQLSMVGLFQRIVSKEGVSGLYRGITPNFMKVLPAVGISYV
VYENMKQTLGVAQK"
262 g 293 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Mus musculus"
/db_xref="taxon:10000"
/clone="IMAGE:4208509"
/tissue_type="Colon, normal. 5
/clone_lib="NCI_CGAP_CO24"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Vector:
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79.1%;
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IMAGE:4208509,
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Pred. No. 4.6e
0; Mismatches
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                                                                                                                                                                                              657.2; DB 10;
No. 4.6e-113;
smatches 203;
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; Murinae; Mus
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KEYWORDS
SOURCE
ORGANISM
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VERSION
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DEFINITION LOCUS

BC019978 Mus musculus, S IMAGE:4239441,

Similar to

2555 bp ar to KIAA1896 , complete cds.

protein,

clone MGC:28954

22-JAN-2002

MGC

BC019978 BC019978.1 house mouse musculus

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Mammalia; E
1 (bases 1
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Submitted (19-DEC-2001) National Institutes of Health, Mammalian Submitted (MGC), Cancer Genomics Office, National Cancer Gene Collection (MGC), Cancer Genomics Office, National Cancer Tractitute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Clone distribution: MGC clone distribution information can be fo
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAK Plate: 37 Row: m Column: 7
This clone was selected for full length sequencing because it
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Web site: http://www.hgsc.bcm.tmc.edu/cdna/contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Huly
Yoon, V.S., Kowis, C.R., Lawrence, S., Mart
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (DNA Sequencing by: Baylor College of Medicine Human Sequencing Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 USA

NIH-MGC Project URL: http://mgc

Contact: MGC help desk

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Jeffrey E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              passed
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center code: BCM-HGSC
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nilarity 64.9%;
Conservative
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YEQMKRLVGSDQETLRHERLVAGSLAGAIAQSSIYPMEVLKTEMALRKTGQYSGMLD
CARRILAKEGVAAFYKGYIPNMLGIIPYAGIDLAVYETLKNTWLQRYAVNSADFGVFV
LLACGTISSTCQQLASY PLALVRTWQQQASIEGAPEVTMSSLFKQIIRTEGAPGLYR
GLAPNFMKVIPAVSISYVVYENLKITLGVQSR"

8 675 c 713 g 582 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GenomeScan gene prediction.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="Similar to KIA./protein_id="AAH19978.1"
/db_xref="GI:18043565"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="MCC:28954 IMAGE:4239441"
/tlssue_type="Kidney, normal. 5 r
/clone_lib="MCI_GGAP_Kid14"
/lab_host="DH10B"
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/db_xref="taxon:10090"
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                                                                                                                                                                                                                                                                                       Score 545.4; DB 1
Pred. No. 4.7e-92;
0; Mismatches 436
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TITLE
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Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium
DNA Sequencing by: Genome Sequence Centre,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Clone distribution: MGC clone distribution through the I.M.A.G.E. Consortium/LLNL at: Series: IRAK Plate: 57 Row: e Column: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield, Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin, Letticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott, Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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GLAPNFMKVIPAVSISYVVYENLKITLGVQSR"
a 675 c 710 g 567 t
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PLDRLKVLMQVHASRSUNMCIVGGFTQNIREGCAKSLWRGNGINVLKIAPESAIKFMA
YEQMKRLVGBOQETLRIHERLVAGSLAGAIAGSSIYFWEVLKTEMALRKTGQYSGMLD
CARRILAKEGVAAFYKGYIPMLGIIFYAGIDLAVYETLKNTWLQRYAVNSADPGVFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="Liver, normal.
/clone_lib="NCI_CGAP_Li9"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="Unknown (protein for MGC:36388)"
/protein_id="AAH22114.1"
/db_xref="GI:18380992"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                 translation="MQSLRDLGVKISEQQAEKILKSMDKNGTMTIDWNEWRDYHLLHP/
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                                                                                                                            20.4%;
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                                                                                                    Score 545.4; DB 10;
Pred. No. 4.7e-92;
0; Mismatches 436;
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Cancer Genomics Office, National Cancer
rive, Room 11A03, Bethesda, MD 20892-2590,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Eukaryota: Metazoa: Chordata: Craniai Mammalia: Eutheria; Primates: Catarri 1 (bases 1 to 3712)
Nagase, T., Kikuno, R. and Ohara, O. Prediction of the coding sequences o: XXI. The complete sequences of 60 new code for large proteins
DNA research: an international journ reports on genes and genomes. 8 (4), Homo sapiens mRNA for KIAA1896 p. AB067483 Homo sapiens brain cDNA to (bases ara,O., 1 to 3712) Nagase, T. a and Kikuno mRNA, Craniata; Vertebrata; Catarrhini; Hominidae. protein, journal for rapid p (4), 179-187 (2001) clone:fk06388 s of unidentified cDNA clones f partial Hominidae; linear cds from publication human Euteleostomi; brain 15-SEP-2001 of

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Submitted (27-JUL-2001) Osamu Ohara, Kazusa DNA Research Institute,
Department of Human Gene Research; 1532-3, Yana, Kisarazu, Chiba
292-0812, Japan (E-mail:cdnainfo@kazusa.or.jp,
URL:http://www.kazusa.or.jp/huge, Tel:81-438-52-3913,
Fax:81-438-52-3914)
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Similarity 63.1%;
05; Conservative
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AQSSIYPMEVLKTRMALRKTGQYSGMLDCARRILAREGYAAFYEGYVPNNLGIIPYAG
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SIEGAPEVTMSSLFKHILRTEGAFGLYRGLAPNFMKVIPAVSISYVVYENLKITLGVQ
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<206. .1912
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/db_xref="taxon:9606"
/clone="fk06388"
/tissue_type="brain"
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VEERQTGMMWRHLVAGGGAGAVSRTCTAPLDRLKVLMQVHASRSNNMGIVGGFTQMIR
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HYLQDHEKKLRLVFKSLDKKNDGRIDAQEIMQSLRDLGVKISEQQAEKILKRIRTGHF
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206. .1912
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/codon_start=1
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                                                                                                                                                                                         AK054901 2857 bp mRNA linear PRI 31-OCT-2 Homo sapiens cDNA FLJ30339 fis, clone BRACE2007401, moderately similar to Oryctolagus cuniculus peroxisomal Ca-dependent solute
                                                                     Homo sapiens
                                 Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                              carrier mRNA.
                  (sites)
Yamazaki, M.,
                                 Chordata;
Primates;
Watanabe, K.,
                                 Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                      clone_lib:BRACE2
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NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fukuzumi,Y., Fujimori,Y., Komiyama,M., Sugiyama,T., Irie,R., Otsuki,T., Sato,H., Wakamatsu,A., Isiii,S., Yamamoto,J., Isono Kawai-Hio,Y., Saito,K., Mishikawa,T., Kimura,K., Yamashita,H., Matsuo,K., Nakamura,Y., Sekine,M., Kikuchi,H., Kanda,K., Magatsuma,M., Murakawa,K., Kanehori,K., Takahashi-Fujii,A., Oshima,A., Sugiyama,A., Kawakami,B., Suzuki,Y., Sugano,S., Nagahari,K., Masuho,Y., Nagai,K., and Isogai,T.
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Submitted (24-OCT-2001) Takao Isogai, Helix Research Institute,
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Chordata;
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                                 AAGCAGCTGGTGGCCGCGCGCAGTGGCAGGTGCCGTGTCACGGACAGGCACGGCCCCTCTG
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YRGYLPNMLGIIPYACTDLAVYEMLQCFWVKSGRDMGDPSGLVSLSSVTLSTTCGQMA
SYPLTLVRTRMQAQGQPVPSGHHACPFPAPPWLSQFSHTPKLSPAPSVSDPSPLLITF
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/db_xref="GI:18128717"
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/db_xref="taxon:9606"
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Wiemann,S., Weil,B., Wellenreuther,R., Gassenhuber,J., Glassl
Ansorge,W., Boecher,M., Bloecker,H., Bauersachs,S., Blum,H.,
Lauber,J., Duesterhoeft,A., Beyer,A., Koehrer,K., Strack,N.,
Mewes,H.W., Ottenwaelder,B., Obermaier,B., Tampe,J., Heubner,
Mambutt,R., Korn,B., Klein,M. and Poustka,A.
Toward a Catalog of Human Genes and Proteins: Sequencing and
Analysis of 500 Novel Complete Protein Coding Human cDNAs
Genome Res. 11 (3), 422-435 (2001)
Martinsried, GERMANY
Clone from S. Wiemann, Molecular Genome Analysis, German Ca
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
                                                Submitted (15-MAY-1999) MIPS,
                                                             Ansorge, W., Wirkner, U., Direct Submission
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DKFZp586G0123
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                                                Am Klopferspitz 18a,
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                 German Cancer
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433; Conserv
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This clone (DKFZp586G0123) is available at the RZPD in Berlin Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 140 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further information about the clone and the sequencing project is available.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    http://www.mips.biochem.mpg.de/proj/cDNA/.
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/translation="MKLYLFQWALFHFTTVPLFGSWSYTLIFSILLLNYQHKAIYLKD
SVYPAIALKSSRKRNPLTCISFCRASLFSFVLCFLPFESDSVLVRKTSWDHS"
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/protein_id="CAB62534.1"
/db_xref="GI:6562166"
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25. .315
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/clone_lib="586 (synonym: hute1). Vector pSport1;
DH10B; sites NotI + Sall/MluI"
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/db_xref="taxon:9606"
/clone="DKFZp586G0123"
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                     ctgcccctttggaccgtctgaaaatcatgatgcaggttcacggttcaaaatcagacaaaa 831
                                                                                                                  gacaatggtggaggcagcttttggcaggaggcattgctggtgctgtctctcgaacaagca 771
                                                                                                                                                                                  TIGATGTGGGTGAGAATCTAACGGTCCCGGATGAGTTCACAGTGGAGAGGGAGAGGCAGACGG
CGGCCCCCTGGACAGGCTCAAGGTGCTCATGCAGGTCCATGCCTCCCGCAGCAACAACA
                                                                                       GGATGTGGTGGAGACACCTGGTGGCAGGAGGTGGGGCCAGGGGCCGTATCCAGAACCTGCA
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Direct Submission
Submitted (26-MAR-2001) National Institutes of Health, Mammalian Submitted (MGC), Cancer Genomics Office, National Cancer Gene Collection (MGC), Cancer Genomics Office, National Cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2757 bp
Homo sapiens, clone IMAGE:3530123,
BC005163
BC005163.1 GI:13477372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Clone distribution: MGC clone distribution information can be for through the I.M.A.G.B. Consortium/LLNL at: http://lmage.llnl.gov Series: IRAL Plate: 11 Row: e Column: 21
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cDNA Library Preparation: Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LL DNA Sequencing by: Institute for Systems Biology http://www.systemsbiology.org contact: amadan@systemsbiology.org Anup Madan, Rachel Dickhoff, Jessica Fahey, Stephanie Greene, Mark Ketteman and Anuradha Madan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  passed the following selection criteria: analysis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Strausberg, R.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                  /Product="Unknown (protein for IMAGE:3530123)"
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a 710 c 843 g 605 t
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Pred. No. 4.6e-62;
0; Mismatches 326;
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                                                                                                                                                                               AX340224
Sequence 471 from
AX340224
                                                                                                 Homo sapiens
Eukaryota; Metazoa;
Mammalia; Eutheria;
                    cancer
Patent: WO 0196388-A 471 20-DEC-2001;
CORIXA CORPORATION (US)
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Jiang,Y., !
                                                              Compositions
                                                                                                                                           human.
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Primates;
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                                                           and Secrist, H. for the therapy
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a 98 c 88 g 22
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96.0%;
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Pred. No. 3.2
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Search completed: August 18, Job time: 19296 sec 2002, 08:23:49

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Maximum DB seq length: 2000000000
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1: /SIDS1/gcgdata/gc2: /SIDS1/gcgdata/gc3: /SIDS1/gcgdata/gc5: /SIDS1/gcgdata/gc5: /SIDS1/gcgdata/gc6: /SIDS1/gcgdata/gc7: /SIDS1/gcgdata/gc9: /SIDS1/gcgdata/gc9: /SIDS1/gcgdata/gc9: /SIDS1/gcgdata/gc1: /SIDS1/gcgdata/gc2: /SID
I: SIDS1/gcgdata/geneseq/geneseqn-embl/NA1980.DAT: *
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SUMMARIE

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ALIGNMENTS

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AAK52210
ID AAK52210;
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AC AAK52210;
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C AAK52210;
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DT 06-NOV-2001 (first entry)
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DE Human polynucleotide SEQ ID NO 755.
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W Vaccine; peptide therapy; stem cell differentiation; gene therapy;
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dermatological; neuroprotective; thrombolytic; coagulant; vasotropic; antipsoriatic; antianglogenic; gene therapy; i immune disorder; haematopoietic cell disorder; autoimmune allergic reaction; graft versus host disease; organ reject haemostatic; thrombolytic; cardiovascular disorder; infect neurological disease; drug screening; ss.
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C. AAC77607 to AAC78448 encode the human cancer associated proteins given in AAB43398 to AAB4239. The proteins can have activities based on the Ct issues and cells the genes are expressed in. Example of activities include: cytostatic; proliferative; vulnerary; immunomodulator; contides cytostatic; proliferative; vulnerary; immunomodulator; cantidiabetic; antiasthmatic; antirheumatic; antiarthritic; antivinfal; antivinfal; antivinfal; antivinfal; antivinfal; antivinfal; antivinfal; coagulant; concurrence cytostopic; vasotropic; antipsoriatic and antiangiogenic. The polynucleotides and polypeptides can be used for preventing, treating or coameliorating medical conditions and diagnosing pathological conditions. Cytoplynucleotides, polypeptides, antibodies, agonists and antagonists from the present invention may be used to treat immune disorders by activating complications. The present invention of the present inventions, differentiation or mobilisation of immune cells, to treat disorders of haematopoietic cells, autoimmune completed in the proliferation of the present inventions. The peptides, nucleotides, antibodies, agonists and antagonists may be also be used in drug screens. AAC78449 to the present invention.

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Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to human polynucleotides (AAI63803-AAI64012) and the encoded proteins (AAM434497-AAM43660) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes were isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland,
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2000US-02118890.
2000US-02118290.
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                                                                                                                                                         The present invention relates to the isolation of novel human CC calcium-binding proteins (AAU19892-AAU19969), and cDNA and genomic CC sequences encoding for these proteins. The sequences of the invention CC are useful in the diagnosis, prevention and/or prognosis of diseases (consociated with aberrant calcium flux. Such disorders include CC neurological diseases (e.g. amylotrophic lateral sclerosis, ALS), CC immune dysfunction (e.g. severe combined immunodeficiency, SCID), CC disease (e.g. cancer), blood disorders (e.g. haemophilia), and/or CC disease (e.g. cancer), blood disorders (e.g. haemophilia), and/or CC infectious disease (e.g. acquired immunodeficiency syndrome, AIDS). The CC calcium-binding proteins are also useful as screening tools to CC identify antagonists and/or agonists that may enhance or inhibit CC activities mediated by calcium-binding proteins. The polynucleotides of the invention are also useful in gene therapy. AAS31577-AAS31654 CC represent cDNA sequences encoding for the novel human calcium-binding
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Matches 826; Conservative
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09-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  epithelial cells, inhibiting the binding of human immunodeficiency virus (HIV)-1 to leukocytes, and treating inflammatory disease, cancer and neurological diseases. The polynucleotide can be used as a marker, in the identification of genetic disorders, and for the design of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1;
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vulnerary; immunomodulatory; vaccine;
tion; cancer; angiogenesis inhibition;
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RESULT AAZ61789 ID AAZ6 XX AAZ6 AC AAZ6 XX CAAZ6 XX CDNA XX Skin XW Secr AAZ61789 standard; cDNA; 1816

27-MAR-2000 (first

cDNA encoding murine ADP/ATP transporter family protein, SEQ ij NO:262

Skin; dermal papilla; keratinocyte; neonatal foreskin fibroblast; embryonic skin cell; keratinocyte stem cell; transit amplifying c secreted; transmembrane; inflammation; cancer; neurological disea transit amplifying cell r; neurological disease; cell;

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                                                                                                                                                                                                                                                                                                                                                                                          CC The invention relates to novel nucleic acid sequences derived from rat CC dermal papilla, human keratinocytes and meonatal foreskin fibroblasts, CC and mouse embryonic skin, keratinocyte stem cells and transit amplifying CC cells. Polypeptides of the invention may be used to treat inflammation, CC cancer and neurological diseases. The proteins may be used to stimulate CC the growth and motility of keratinocytes, to inhibit the growth of CC cancer cells, to modulate angiogenesis and tumour vascularisation, to modulate skin inflammation, to modulate epithelial cell growth and to CC inhibit binding of HIV-1 to leukocytes. The invention may also be used to treat growth and developmental defects, skin wounds and hair follicle CC disorders. Sequences AAZ61606-Z61832 represent cDNA sequences derived CC from several mouse, rat or human skin cell types. Sequences derived CC AAZ61606-Z61649, AAZ61725-Z61785, AAZ61802-Z61811 and AAZ61826 encode proteins with an N-terminal signal sequence, indicating that the proteins are secreted. Sequences AAZ61650-Z61668, AAZ6176-Z61780, AAZ61812-Z61817 can semembrane domains.
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                      tgaccatcgactggaacgagtggagggactaccacctcctgcaccctgtggagaacatcc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim
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AAZ65058 standard; CDNA; 3333 ВP

AAZ65058

05-APR-2000 (first entry)

Membrane-bound protein PRO1106 encoding

Membrane-bound pharmaceutical; polypeptide; PRO polypeptide;
; receptor immunoadhesin; gene LDL receptor; TIE

mapping;

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99US-0169495.
99US-0170262.
2000US-0175481.
2000WO-US04341.
2000WO-US04342.
2000WO-US04414.
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2000WO-US08439
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99WO-US12252. 99US-0141037. 99US-0143048.

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                                                                                                                                                                                                                                         Matches
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26-JUL-1999

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Ferrara N,
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                    aaaataatgatggaaaaattgaggcttcagaaattgtccagtctctccagacactgggtc
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N, Fong S, Gerber H, Gerritsen ME, Goddard
CJ, Gurney AL, Kljavin IJ, Napier MA, Pan
Stewart TA, Tumas D, Watanabe CK, Williams
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2000W0-US30219
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2000W0-US94414
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Pred. No. 4.1e-112;
D; Mismatches 437;
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                tcagctacgtggtctacgagaacctgaagatcaccctgggcgt
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27-APR-2000;
20-JUN-2000;
19-JUL-2000;
01-SEP-2000;
15-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  activity, tissue growth factor activity, immunomodulatory activity and activin/inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis an
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542; Conserv
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2000US-0560875.

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2000US-0598075.

2000US-0620325.

2000US-0634936.

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2000US-0728422.
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J, Zhang J, N.
T, Goodrich J
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28-FEB-2000; 18-MAY-2000; 17-JUN-2000; 14-JUL-2000; 19-SEP-2000;

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HYSEQ

07-SEP-2001

26-FEB-2001;

2001WO-US04926

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                                                                                                                                                                                                                                  antibacterial; immunosuppressive; vasotropic; antiparkinsonian;
neuroprotective; osteopathic; antidiabetic; antiasthmatic; anti
immunostimulant; analgesic; gene therapy.
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cc human, dog, monkey, mouse, hamster or rat. The disorders include cancers cc such as leukaemia, lymphoma and neuroblastoma, autoimmune disorders such cc as multiple sclerosis, connective tissue disease, include cancers cc disorders such as parkinson's disease, Alzheimer's disease, Huntington's connective tissue disease, nervous system cc disorders such as parkinson's disease, Alzheimer's disease, Huntington's cc chorea, amyotrophic lateral sclerosis, spinal muscular atrophy and cc Wernicke disease, inflammatory disorders such as nephritis, Crohn's cc disease, ischaemia-reperfusion injury, shock, sepsis and inflammatory cc bowel disease. The sequences exhibit activity relating to angiogenesis, cell proliferation, cell differentiation, stem cell growth factor, cc activin or inhibin. Therefore, they can be used to manipulate stem cells in culture to give rise to neuroepithelial cells that can be used to cartilage, tendons and ligaments and in tissue repair and burn healing. Cc wote: Some sequences for this patent did not form part of the printed specification, but were obtained in electronic format directly from WIPO cat fire.
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18-MAY-2000;
17-JUN-2000;
14-JUL-2000;
19-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequences AAS44576-AAS44919 represent full-length polynuclectides and contil polynuclectides encoding polypeptides of the invention. The DN and protein sequences are useful for the treatment, diagnosis and prevention of various types of disorder in a mammalian subject such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel polypeptides and nucleic acids obtained from cDNA libraries prepared from various human tissues, for diagnosis, treatment of cancer, neurological, inflammatory disorders and for use in array.
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P-PSDB; AAU27869.
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05-APR-1999;
30-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant; immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antidiabetic; hypotensive; dermatological; immunosuppressive; antidiabetic; antitianatory; antibacterial; antifungal; antirheumatic; antithyroid; antianaemic; gene therapy; cancer; proliferative disorder; hypertension; neurodegenerative disorder; osteoarthritis; graft vs host disease; cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS; cholesterial interpretative disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cholesterol ester storage; systemic lupus erythematosus; infection; severe combined immunodeficiency; malaria; autoimmune disorder; asthma; allergy; aplastic anaemia; nocturnal haemoglobhuria; burn; wound; bone damage; cartilage damage; antiinflammatory disease; coagulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1513
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99US-0127636.
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neuroprotective;
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Query Match Best Local Similarity Matches 738; Conser

Conservative

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Mismatches

406;

Indels

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Gaps

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Length 1481;

18.5%;

Score 494.4; DB 21; Pred. No. 3.7e-101;

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CC antidiabetic, hypotensive; dermatological; immunosuppressive; accounting hypotensive; dermatological; antifungal; antirheumatic; cc antiinflammatory; antibacterial; antiviral; antifungal; antirheumatic; cc antiinflammatory; and antianaemic. The sequences can be used for determining cc the presence of or predisposition to, or preventing or treating cc pathological conditions associated with an ORRY-associated disorder. The cc nucleic acids can be used to express ORFX proteins in gene therapy cc vectors. The proteins and nucleic acids may be used to treat cancers, cc proliferative disorders, neurodegenerative disorders, osteoarthritis, cc graft vs host disease, cardiovascular disease, diabetes mellitus, cy typertension, hypothyroidism, cholesterol ester storage, systemic lupus cerythematosus, severe combined immunodeficiency (SCID), AIDS, viral, concernal or fungal infection, malaria, autoimmune disorders, asthma, callergies, aplastic anaemia, burns, wounds, bone and cartilage damage, cc coagulation; to inhibit thrombosis; and as a contraceptive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAC74446 to AAC77606 encode the proteins given in AAB40237 to which represent the human ORFX open reading frames 1 to 3161. sequences have activities such as: cytostatic; hepatotropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                     antipsoriatic; antiparkinsonian; nootropic; neuroprotective;
osteopathic; anticonvulsant; antiarthritic; immunosuppressant;
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Sequence
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316	Query Match Best Local s Matches 807	MESULT 1 US-09-188-930-262 Sequence 262, Application US/09188! Patent No. 6150502 GENERAL INFORMATION: APPLICANT: Watson, James D. APPLICANT: Watson, James D. APPLICANT: Strachan, Lorna APPLICANT: Ontust, Rene APPLICANT: ONTUST, Rene APPLICANT: ONTUST, Rene APPLICANT: MITISON, James Greg TITLE OF INVENTION: Compositions: TITLE OF INVENTION: and Methods F FILE REFERENCE: 11000.1011c1 CURRENT APPLICATION NUMBER: US/09, CURRENT FILING DATE: 1998-11-99 NUMBER OF SEQ ID NOS: 348 SOFTWARE: FASTSEQ for Windows Ver: SEQ ID NO 262 US-09-188-930-262		44 45	42	4 1	39 0	37	თ თ თ	34	ມພ	31	29	28
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Sequence 23, Application US/09188930A
Patent No. 6150502
GENERAL INFORMATION:
APPLICANT: Watson, James D.
APPLICANT: Strachan, Lorna
APPLICANT: Sleeman, Matthew
APPLICANT: Orrust, Rene
APPLICANT: Murison, James Greg
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; TITLE OF INVENTION: Compositions Isolated From Sk.; TITLE OF INVENTION: and Methods For Their Use; FILE REFERENCE: 11000.1011.0
; CURRENT APPLICATION NUMBER: US/09/188,930A; CURRENT FILING DATE: 1998-11-09; NUMBER OF SEQ ID NOS: 348; SOFTWARE: PastSEQ for Windows Version 3.0; SEQ ID NO 23; LENGTH: 997; TYPE: DNA; CORGANISM: mouse US-09-188-930-23
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; LOCATION: 63..116
; IDENTIFICATION METHOD: Von Heijne matrix
; OTHER INFORMATION: SCORE 5.6
; OTHER INFORMATION: SEQ WHFLASFFPRAGC/HG
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LENGTH: 437 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 29,655
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-8550
TELEFAX: (619) 235-0176
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SOFTWARE: WOTO
CURRENT APPLICATION DATA:
CONTROL NUMBER: US/08/905,223
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ORIGINAL SOURCE:
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ATTORNEY/AGENT INFORMATION:
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                                                           400 AGAATGATGGACGCATTGACGCGCAGGAGATCATGCAG 437
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TYPE: NUCLEIC ACID
STRANDEDNESS: DOUBLE
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                                                                                                                        TCCATTATCTCCAAGATCATGAGAAGAAGCTGAGGCTGGTGTTTAAGAGTTTGGACAAAA 399
                                                                                                                                        tgaagtaccttaaagaccatgagaagaaaatgaaattggcatttaagagtttagacaaaa 438
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: California
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Israelsen, Ned A.
Israelsen, 29,655
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IBM PC compati
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APPLICANT: DORNER
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                                                                                                                                                                                                            1404
                               1344
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NAME: BENT, Stephen A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
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APPLICATION NUMBER:
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493 gtctgactatttctgaacaacaagcagagttgattcttcaaagcattgatgttgatggga 552
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                                                                                                                                                                                                                                                                                               193 agcagccgacgcgctacgagaccctcttccaggcactggaccgcaatggggacggagtgg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: FILING DATE: 26-AUG
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OPERATING SYSTEM:
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                                                                                         tggacatcggcgagctgcaggagggctcaggaacctgggcatccctctgggccaggacg
                                                                                                                                                                                                                                                                                                                                15;
                                                                                                                                                                                                                                                                                                                             h 2.1%; Score 55.8; DB 1; Similarity 3.8%; Pred. No. 0.00027; Similarity 222; Mismatches 154;
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VENTION: RECOMBINANT FOWLPOX VIRUS
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(703)683-4109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DORNER, F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
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US-08-487-826B-13
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Best Local :
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INFORMATION FOR SEQ ID NO:
                                                                                                                         17469 GATATATATGTGGATCATAATAATGTGACTAATAATAATATGGATGTACCTACTAAAATG 17528
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APPLICANT:
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LENGTH: 19124 base pai
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MEDIUM TYPE: Floppy disk
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APPLICANT: Wellems, Thomas E.
TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: NIH121.001CP1
TELECOMMUNICATION INFORMATION:
TELLEPHONE: (619) 235-8550
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CLASSIFICATION: 435
                                                                                                                                                                                       Local Similarity
nes 236; Conserv
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                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Israelsen, Nec
REGISTRATION NUMBER:
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                tctgaaaatgtactggcttgaacaaaatttgtttttgtgtgtttagagttataaatcattaa 1903
                                                                                        cacacaattatactttatctttcttaataatcctgcaaatctctgccctgaatccgaaa 1843
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Chitnis, Chetan
Miller, Louis H.
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                                                                                                                                                                                    Score 53; DB 2; Length 19124; Pred. No. 0.0025; 0; Mismatches 285; Indels
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Patent No. 5965397
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APPLICANT: Jacobs, Kenneth
APPLICANT: MCCOY, John M.
APPLICANT: LaVallie, Edward
                                                                                                                  TELEFAX: (617) 876-58 INFORMATION FOR SEQ ID NO:
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                                                                                                                                  TELECOMMUNICATION INFORMATION: TELEPHONE: (617) 498-8284
TELEFAX: (617) 876-5851
                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION: NAME: Sprunger, Suzanne
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                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2204 tcctggagttatacactaattttcagtatattactgttaaatt 2246
                MOLECULE TYPE:
                                                                                                  SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                         NAME: Sprunger, Suzanne A. REGISTRATION NUMBER: 41,323
                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: U
ZIP: 02140
                                TOPOLOGY:
                                             STRANDEDNESS:
                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE:
                                                                                 LENGTH:
                                                                                                                                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
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                                                        : 2447 base pairs nucleic acid
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Treacy, Maurice
Spaulding, Viki
Agostino, Michael J.
NVENTION: SECRETED PRO
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87 CambridgePark Drive
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Best Local S
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                                                                                                                                                                                          TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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                                                                                                     MOLECULE TYPE: I
                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: F10ppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                             FEATURE:
NAME/KEY:
                                                                                                                                                                                                                                                            NAME: Feeney, Joanne Longo
REGISTRATION NUMBER: 35,134
REFERENCE, DOCKET NUMBER: RIG
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5389526ris
STREET: One Liberty Place 46th Floor
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APPLICATION NUMBER: PCT/AU90/00530
FILING DATE: 02 NOV-1989
ATTORNEY/AGENT INFORMATION:
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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                                                                                                                                   STRANDEDNESS: S1
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                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US
FILING DATE: 19920625
                                                           LOCATION:
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TELEFAX: 215-568-3439
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                                                                                                                                                           1: 5852 base pairs
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Williams, Kei
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Patent No. 6168954
                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 33
LENGTH: 1117
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                                                                                                                                                                                                                                                                                                                                    LOCATION: (1101)
OTHER INFORMATION: NAME/KEY: unsure
LOCATION: (1104)
OTHER INFORMATION: N
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CURRENT APPLICATION NUMBER: US/09/247,373B
CURRENT FILING DATE: 1999-02-10
PRIOR APPLICATION NUMBER: 08/924,747
PRIOR FILING DATE: 1997-09-05
NUMBER OF SEQ ID NOS: 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: MCGONIGLE, BRIAN
APPLICANT: O'KEFFE, DANIEL
APPLICANT: O'KEFFE, DANIEL
TITLE OF INVENTION: SOYBEAN GLUTATHIONE-S-TRANSFERASE ENZYMES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE:
                                                                                                                                                                                                                                                                                              NAME/KEY: unsure LOCATION: (1116) OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: SOYBEAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
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NAME/KEY: unsure
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Pred. No. 0.0019;
2; Mismatches 91;
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US-07-867-106-4
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Patent No. 5389526
GEMERAL INFORMATION:
                                                                                                                                                                                                                                                                                              Query Match 1.9%;
Best Local Similarity 50.4%;
Matches 123; Conservative
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                                                                                                  1985
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FILING DATE: 19920625
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PJ 7187
APPLICATION NUMBER: PCT/AU90/00530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. STREET: One Liberty Place 46th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Slade, Mar
APPLICANT: Chang, And
APPLICANT: Williams,
                                  2045
                                                                   2026
                                                                                                                                                                                   1906 tttatttcgggtggtttacgtttatgccagttcctttatattttaaatttcttgttttata 1965
                                                                                                                                                                                                                                   1865 TTAAAAAACTTGGGTTGGTTAATTATTATTTGAAAATTTTAAAACCCAAATTAAAAAAA 1924
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 3138 base pairs
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 2086 tatt 2089
                                                                                                                                   1966
                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: NUCLEIC ACID STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Feeney, Joanne Longo
REGISTRATION NUMBER: 35,134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC
OPERATING SYSTEM:
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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Andy C M
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Improved Plasmid Vectors for Cellular
Slime Moulds of the Genus Dictyostelium
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; Sequence 13, Appl
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Matches
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                                                                                                                                                                                                                                                                                                                 Query Match
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                                                                                                                                                                                                                  15657
                                                                                                                                                                                                                                       1871 tttgttttgtgtgttagagttataaatcattaatctttatttcgggtggtttacgtttat 1930
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-8550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,826B
FILING DATE: 10-SEP-1993
CLASSIFICATION: 435
CLASSIFICATION: 435
CLASSIFICATION: 435
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MEDIUM TYPE: Floppy disk
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                  2051 caaaagcatccaaataagtatagggtttatgtccttatttttcttt 2096
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HYPOTHETICAL:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: sing
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Chitnis, Chetan
Miller, Louis H.
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Wellems, Thomas E.
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AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
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0; Mismatches
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Patent No.
                                                                                                                                                                                                                                                               Matches 144;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: JP 433
FILING DATE: 28-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/
FILING DATE: 01-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: WHITE JR., PAUL E
REGISTRATION NUMBER: 32,01
                                                                                                                                                           1921 ttacgtttatgccagttcctttatattttaaatttcttgttttatatattttgaatgtctt 1980
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 861-3000
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
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                      TCTTTTCCATCATCATCATCATCATCACGAGTTTTCGGTTATCAATACTCTTTTCAT 936
                                                                 tatagatttctttaaatttccttatagaaccattaatagaaaatcattacatttaaaata 2040
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                                                                                                                                                                                                                                                                                                                                                                                            nucleic acid
DEDNESS: double
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20005-3918
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IVENTION: NOVEL VECTOR HAVING PROMOTER THAT IS
IVENTION: INDUCIBLE BY METHANOL AND/OR GLYCEROL
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SHIBANO, YUJI
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SYSTEM: PC-DOS/MS-DOS
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)N: 435
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Pred. No. 0.004;
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RESULT 12
US-08-343-428-1
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US-08-343-428-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Haley, Jr., James F.
REGISTRATION NUMBER: 27794
REFERENCE/DOCKET NUMBER: SH
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 19-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: Haley, Jr., James
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 18-NOV-: CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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ADDRESSEE: James F. Haley, Jr., Fissers STREET: 1251 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
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ORIGINAL SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
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APPLICATION NUMBER: P
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OPERATING SYSTEM:
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                                                                                             NAME/KEY:
                                                                                                                        IDENTIFICATION
                                                                                                                                                      LOCATION:
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                          [DENTIFICATION
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10020-1104
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INVENTION: No. 5665586el Protease
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Tsuzuki, Hiroshige
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                                                        METHOD:
peptide
5..944
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US-08-998-416-1137
; Sequence 1137, Application US/08998416
; Patent No. 6239264
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Best Local
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                 INFORMATION FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
                                          NAME: Meigs, J. Timothy
REGISTRACION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8587
                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                       SOFTWARE: Patentin Rel-
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: ĞENOMIC DNA SEQUITITLE OF INVENTION: AND USES THEREOF NUMBER OF SEQUENCES: 1152
                                                                                                                          FILING DATE: 31-DEC-1996 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                           CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS
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CITY: Research Triangle Park
STATE: No. 6239264th Carolina
                            TELEFAX:
                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
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                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                           APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION:
                                                                                                                                                                                                                                                                                                                                            27709
CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                           USA
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Knechtle, Philipp
Rebischung, Corinne
REPORTION: GENOMIC DNA SEQUENCES
                                919-541-8689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Philippsen, Pete
Pohlmann, Rainer
Steiner, Sabine
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                 SEQ ID
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N: 435
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RESULT 14
US-07-945-283-1
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                                                                                                                                                                            Sequence 1, Application US/07945283
Patent No. 5352596
GENERAL INFORMATION:
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Best Local Similarity
Matches 261; Conserv
COMPUTER READABLE
                                                                                                                       APPLICANT: Cheung, Andrew K.
APPLICANT: Wesley, Ronald D.
TITLE OF INVENTION: Pseudora
TITLE OF INVENTION: Involvin
                                                                                            CORRESPONDENCE ADDRESS:
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ORIGINAL SOURCE:
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                                                                                                            NUMBER OF SEQUENCES:
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             COUNTRY: UZIP: 61604
                                                     STREET: 1815
CITY: Peoria
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                                          STATE:
                                                                                 ADDRESSEE:
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                                                                                                                                                                                                                                                                                                        ttactgttaaattaccaacacaaggcaatttatttgaa
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                                       ΙL
                                                                    1815 No.
                           USA
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                                                                                 Curtis P. Ribando
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FORM:
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                                                                  5352596th University
                                                                                                                        Involving
                                                                                                                                     Pseudorabies Virus Deletion Mutants
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CURRENT APPLICATION DATA:

APPLICATION NUMBER:

US/07/945,283

19920911

OPERATING SYSTEM: F SOFTWARE: PatentIn

compatible
PC-DOS/MS-DOS
In Release #1.0, Version #1.25

MEDIUM TYPE:

IBM PC

Floppy disk

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US-08-998-416-186

; Sequence 186, Application US/08998416

; Patent No. 6239264

; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                    Matches 108;
                                                                                                                                                                                                                                                                                                          Query Match
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INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                       4493
                                                                                                                                                                                          4553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 27976
TELECOMMUNICATION INFORMATION:
TELEPHONE: 309-685-4011 ext.513
                                                                                             4673 CGCTCGAGGACGCCGCGGCAGGCCAGGA 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE HYPOTHETICAL: P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 8438 base pair
   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
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                                                                                                                 292 gcatccctctgggccaggacgccgagga 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 19
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
1818
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ORIGINAL SOURCE:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8587
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FILING DATE: 31-DEC-1196
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
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MEDIUM TYPE: Floppy
                                                                                                                                              1878
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T: 3054 Cornwallis Road
Research Triangle Park
No. 6239264th Carolina
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Search completed: August 18, 2002, 08:14:03 Job time: 17844 sec

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BASE COUNT 1020 bp mRNA linear E AGENCOURT_6393362 NIH_MGC_72 Homo sapiens cDNA clone 5', mRNA sequence. BM450214 Contact: Robert Strausberg, Ph.D. Email: cgapbs-remail.nih.gov Tissue Procurement: ATCC/DCTD/DTP High quality sequence stop: 619. Location/Qualifiers found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLAM12204 row: o column: 10 NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates; 1 (bases 1 to 1020) Homo sapiens EST BM450214.1 human. cDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can 315 Ω /tissue_type="melanotic melanoma" /lab_host="DH10B (phage-resistant)" /note="Organ: skin; Vector: persistant) Site_2: Sall; Cloned unidirectionally. Primer: Oligo (Average insert size 2 kb. Library constructed by Life Technologies." /organism="Homo sapiens" /db_xref="taxon:9606" /clone="IMAGE:5528289" /clone_lib="NIH_MGC_72" GI:18499254 269 g Craniata; Vertebrata; Catarrhini; Hominidae; 253 Library constructed by Life Euteleostomi; Homo. EST 05-FEB-2002 e IMAGE:5528289 þe

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Contact: Robert Strausberg, |
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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National Institutes of Health, Mammalian
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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National Institutes of Health, Mammalian Gene Collection (Matting Institutes of Health, Mammalian Gene Collection (Matting Institutes of Health, Mammalian Gene Collection (Matting Institutes)
L Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Aaron Hsueh
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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       /organism="Mus musculus"
//db_xref="taxon:10090"
/clone="IMAGE:5504225"
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/lab_host="DH10B (Tl phage-resistant)"
/lab_host="DH10B (Tl phage-resistant)"
/not="Organ: ovary, PMSG-treated; Vector:
/note="Organ: ovary, PMSG-treated; Vector:
pCMV-SPORT6.ccdb; Site_1: EcoRV; Site_2: NotI; Cloned
unddirectionally. Primer: Oligo dT. Average insert size
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Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Gemomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suchiro-cho, Tsurumi-ku, Yokoham Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp,
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1674 bp mRNA linear HTC 19-JAN-2002

Mus musculus adult male testis cDNA, RIKEN full-length enriched

library, clone:4930443G12:homolog to PEROXISOMAL CA-DEPENDENT
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/protein_id="Bab29816.1"
/db_xref="G1:12853685"
/fdmxref="G1:12853685"
/franslation="MLRLQDFLLPSEACQNDYNRLAYEVLPEDLDHNGDGVVDITEL
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DIVRFWKHSTIIDIGESISIDEFTEDEKMSCEWMKRLVAAGIASATTRTCTAPLERL
KVTMQVOSLKVNKMGLYMHFKQMVKEGGFFSGFSWYKRLVAAGIASATIKIGAYEQYL
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KLLSPDGDHLGVLQFTAGCMAGATSOTCVPDMEVIKTRLNLSKTGEYSGLVDCVRKY
KLLSPDGDHCSVLQFUAGCMAGATSOTCVPMEVIKTRLNLSKTGEXGGLVGCS
TYSHTCGQLASEPLILVRTRMQAVMLEKETVRMMQLIQEIYTKEGKKGFFRGFTPNVL
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78. .1499
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/strain="C57BL/6J"
/db_xref="MGD:MGI:1907887"
/db_xref="taxon:10090"
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/clone_lib="RIKEN full-length enriched mouse cDNA library"
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BE731210
BE731210.1 GI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                        /tissue_type="choriocarcinoma"
//lab_host="DHIOB (phage resistant)"
/lab_host="DHIOB (phage resistant)"
/note="Organ: placenta; Vector: pOTB7; Site_1: XhoI;
/note="Organ: placenta; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the following 5 adaptor: GGCAGGAGG(). Size-selected >500bp for average insert size 1.8kb. Library constructed by ling Hong in the laboratory of Gerald M. Rubin (University of Callifornia, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
a 232 c 275 g 211 t
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/clone="IMAGE:3842039"
/clone_lib="NIH_MGC_21"
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Pred. No. 2.3e-91;
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                                                                                             Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, M
Unpublished (1999)
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EST.
 found through the I.M.A.G.E. Consortium/LLNL http://image.llnl.gov Plate: LLCM966 row: g column: 10
                                                                                                                        Contact: Robert Strausberg, Ph.D.
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/clone_lib="NIMGE_54"
/tissue_type="from chronic myelogenous leukemia"
/tissue_type="from chronic myelogenous leukemia"
/lab_host="DHIDB (T1 phage-resistant)"
/lab_host="DHIDB (T1 phage-resistant)"
/note="Organ: bone marrow; Vector: pDNR-LIB (Clontech);
Site_l: Sfil (ggccgctcggc); Site_2: Sfil (ggccattatggcc); Site_1: Sfil (ggccattatggcc); Site_3: Adaptor sequence were used in cloning as follows: 5'
and 3' adaptors were used in cloning as follows: 5'
adaptor sequence: 5'-CACGGCCATTATGCCC-3' and 3' adaptor
sequence: 5'-ATTCTAGAGGCCAATGATGCCGCAATG-dT(30)BN-3'
(where B = A, C, or G and N = A, C, G, or T). Average
insert size 1.75 kb (range 0.9-4.0 kb). 15/15 colonies
contained inserts by PCR. This library was enriched for
full-length clones and was constructed by Clontech
Laboratorles (Palo Alto, CA)."
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                                                                                                                                                                                                                     662;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Chu-Xia Dr.
CDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNI
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAMill67 row: n column: 16
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
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High quality sequence stop: 734.
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/clone="IMAGE:5062095"
                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="tumor, gross tissue"
/lab_host="DH10B"
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                                                                                            MA 02138
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, Jackson,Y. and Bowers,Y.
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TGTACGAGCTTTTGAAGTCTTATCGGCTGGATTAACTTTGCCAAAGACTCGGTCAAACC
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556
ie53b05.yl Melton Normalized cDNA 5' similar to TR:Q9UG66
;, mRNA server B1962667.1 ;, mRNA sequence GI:16337072 bp mRNA linear EST 23-OCT-2001 Human Islet 4 N4-HIS 1 Homo sapiens Q9UG66 HYPOTHETICAL 11.3 KD PROTEIN.

Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo.

Unpublished (2000)
Other_ESTs: ie53b05.x1 Contact: Douglas Melton, Klaus H. Endocrine Pancreas Consortium Kaestner,

Tsagareishvili,R., Williams,T.

Endocrine Pancreas Consortium Harvard University, Howard Hughes Medical Dept of Molecular and Cellular Biology, 7 Divinity A

& Hiroshi

Tel: 617-495-1812 Fax: 617-495-8557

Email: dmelton@biohp.harvard.edu

Library was constructed by Dr. Douglas Melton DNA sequencing by Washington University Genome Sequencing Center For information obtaining a clone please contact: Juliana Brown by: 9

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Location/Qualifiers
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Site_2: Sal 1; Starting library constructed using
SuperScript Plasmid Library kit (Life Technologies). cDNA
made by oligo-dT priming. Size-selected by column
fractionation; average insert size 1.08 kb. Library was
amplified once on solid support and plasmid DNA from
library was prepared. The library DNA was normalized by
method #4 from Bonaldo, Lennon, and Soares 1996 Genome
Research 6:791-806; 0.5 micrograms single-stranded library
plasmid DNA was mixed with 5 micrograms PCR product
representing library inserts and hybridized to an Ecot of
20. Single-stranded (unhybridized) plasmids were isolated
by hydroxyapatite chromatography and used to make this
library."

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/sex="Both"
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gggacggagtggtggacatcggcgagctgcaggaaggggctcaggaacctgggcatccctc
                   tccagacactgggtctgactatttctgaacaacaagcagagttgattcttcaaagcattg
                                                                                                                                                                                     ttaagagtttagacaaaaataatgatggaaaaatttgaggcttcagaaattgtccagtctc
                                                                                                                                                                                                                                                                                                                                                                                                                    ATGTTGATGGGACAATGACAGTGGACTGGAATGAATGGAGAGACTACTTCTTATTTAATC
                                                                                  TCCAGACACTGGGTCTGACTATTTCTGAACAAGCAGGAGTTGATTCTTCAAAGCATTG
                                                                                                                                                                  TTAAGAGTTTAGACAAAATAATGATGGAAAAATTGAGGCTTCAGAAATTGTCCAGTCTC
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German Genome Project.

No Sl sequence available.

No Sl sequence available at the RZPD in This clone (DKFZp313M1729) is available at the RZPD in Please contact the RZPD: Ressourcenzentrum, Heubnerweg Please contact the RZPD: Ressourcenzentrum, GERMANY; Email: clone@rzpd.de.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This is the 5' sequence of the clone insert Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email S. Wiemann@dkfz- heidelberg.de; sequenced by GBF (National Research Centre for Biotechnology Ltd. Braunschweig/Germany) within the cDNA sequencing consortium of th
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DKFZp313M1729_r1 313 (synonym:
DKFZp313M1729 5', mRNA sequenc
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Contact: Bloecker
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/clone_lib="313 (synonym: hlcc2)"
/dev_stage="adult"
/lab_host="DH10B"
/note="Vector: pTriplEx2; Site_1: SfcDNA-collection"
82 c 135 g 122 t
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/db_xref="taxon:9606"
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Pred. No. 8.2e
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1644 tgaaacaagtctatggcaaaagaagctgcatttttttcacaaaagggaagacggtaacaa 1703
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                             tgctttagcctgataattgaaactttcaacaatctctggagtgactttttctcctcgaat 1643
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                                                                                            591;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: ATCC
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
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601645924F1 NIH_MGC_59 Homo sapiens
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                                                                                           Conservative
                                                                                                                                                                                                                   /tissuc_type="muccepidermoid carcinoma"
/lab_host="bH10B (T1 phage-resistant)"
/note="Organ: lung; Vector: pDNR-LIB (Clontech); Site_1:
Sfil (9gccgctcggcc); Site_2: Sfil (9gccattatggcc);
Double-stranded cDNA was prepared from cell line RNA. 5'
and 3' adaptors were used in cloning as follows: 5'
adaptor sequence: 5'-ACGCGCCATTATGGCC-3' and 3' adaptor
sequence: 5'-ACTCTAGAGGCCGACATG-dT(30)BN-3'
(where B = A, C, or G and N = A, C, G, or T). Average
insert size 1.65 kb (range 0.9-4.0 kb). 15/15 colonies
contained inserts by PCR. This library was enriched for
full-length clones and was constructed by Clontech
                                                                                                                                                                               Library.
a 148
                                                                                                                                                                                                             Laboratories (Palo Alto, CA). Note: this is a NIH_MGC
                                                                                                                                                                                                                                                                                                                                                                                                        /clone="IMAGE:4102109"
/clone_lib="NIH_MGC_59"
                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                         Score 493.8; DB 10;
Pred. No. 3.4e-73;
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                                                                                                             found through the I.M.A.G.E. Consortium/LLNL http://image.llnl.gov
http://image.llnl.gov
plate: LLAM9730 row: b column: 08
High quality sequence stop: 534.
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National Institutes of Health, Mammalian
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Mammalia; Eutheria; Primates;
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                                                                                                                                                            (bases 1 to 921)
/organism="Homo sapiens"
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/clone="IMAGE:3912103"
/clone_lib="NIH_MGC_71"
                                                                                             Location/Qualifiers
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BB623288
Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Koud,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M., M., Koya,S., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasak,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T.,
                                                                             Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
1 (bases 1 to 632)
1 (bases 1 to 632)
                                                                                                                                                                                                     duct Mus musculus
BB623288
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RIKEN full-length enriched, 12
musculus cDNA clone 6720455K09
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/lab_host="DH10B (phage-resistant)"
/note="Organ: uterus; Vector: pcMV-SPORT6; Site_1: Not1;
Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2.1 kb. "
a 254 c 239 g 187 t 1 others
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Matches

514;

Conservative

0,

Mismatches

; 1.9e-69; 71;

0;

Gaps

0;

Length

Query Match Best Local Similarity

17.6%; 87.9%;

Score 471.4; Pred. No. 1.9

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BASE COUNT
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JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: genome-resegsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Carninol.p., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., I
,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.,
Normalization and subtraction of cap-trapper selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yonda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuu
,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001) Yamanaka, I., Kiyosawa, H., Kondo, S., Saito, T., Shinagawa, A., Aizaw, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K., Arakawa, T. Ishii, Y. and Hayashizaki, Y. Mapping of 1903 mouse cDNAs on mouse chromosomes. J. Struct. Func. Genomics 2 pre, L72-L86 (2001 Please visit our web site (http://genome.gsc.riken.go.jp) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Laboratory for Genome Exploration Research Group, RIKEN Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-
Tel: 81-45-503-9222
Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequencing pipeline with 384 multicapillary set 10 (11), 1757-1771 (2000) Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Y. and Hayashizaki, Y., Y. and Hayashizaki, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Muramatsu, M. and Hayashizaki,Y. RIKEN Mouse ESTs (Arakawa,T., e Unpublished (2001)
Contact: Yoshihide Hayashizaki
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e mouse tissue
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                          179
                          a
                                                                                                                            was cloned into the XhoI and BamHI sites. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I. Cloning sittes, 5^\circ end: SalI; 3^\circ end: BamHI ^* 149 c 169 g 135 t
                                                                                                                                                                                                                                                                                                                                                                                     prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="wolffian duct includes
/dev_stage="12 days embryo"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="RIKEN full-length enriched,
male wolffian duct"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Site_1: Sall; Site_2: BamHI; cDNA library
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/clone="6720455K09"
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/strain="C57BL/6J"
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PO Box 166, Clay Co
Tel: 402 762 4366
Fax: 402 762 4390
                                                                                                                                                                                                                                                                                     BG894729
355456 MARC 1PIG $
BG894729
BG894729.1 GI:14:
EST.
                                                       Email: smith@email.marc.usda.gov
Single pass sequencing. Bases ca.
v0.980904.e. Vector identified b.
and -minmatch 12 options.
                                                                                                                        EST discovery in swine Unpublished (2000)
Contact: Smith TPL USDA, ARS, US Meat Animal Research Center USDA, ARS, US Meat Animal Research Center USDA, Clay Center, NE 68933-0166, US
                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; 1 (bases 1 to 531)
Fahrenkrug,S.C., Freking,B.A., Rohrer,G.A., Smith,T Stone,R.T., Heaton,M.P., Grosse,W.M., Bennett,G.A., and Keele,J.W.
FORWARD: AGGAAACAGCTATGACCAT
BACKWARD: GTTTTCCCAGTCAGGACG
Plate: 119 row: K column:
Seg primer: ATTTAGGTGACACTATA
                                             and -minmato
PCR PRimers
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 ATTTAGGTGACACTATAG
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Sus scrofa cDNA
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Laegreid,W.W.
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Sus.
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DEFINITION
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                       TITLE
                                                         AUTHORS
                                                                                                      ORGANISM
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355388 MARC 1
BG894680
BG894680.1 (
EST.
                               pig.
Sus scrofa
Eukaryota; Metazoa; Chordata; Cranlata; Vertebrata; Eutele
Eukaryota; Metazoa; Chordata; Cranlata; Vertebrata; Eutele
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
1 (bases 1 to 529)
Fahrenkrug,S.C., Freking,B.A., Rohrer,G.A., Smith,T.P.L.,
Stone,R.T., Heaton,M.P., Grosse,W.M., Bennett,G.A., Laegra
and Keele,J.W.
         Design and use of two pooled tissue normalized cDNA libraries for EST discovery in swine
Unpublished
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/db_xref="taxon:9823"
/clone_lib="mARC 1PIG"
/tissue_type="pooled"
/lab_host="DH10B"
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Library made from pooled tissue from day 11, 13, 1
and 30 embryos."
9 c 140 g 139 t
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91.9%;
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Pred. No. 6.8e
0; Mismatches
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Sus.
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Laegreid,W.W
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                                                                     tgaacagtacaagaagttacttactgaagaaggacaaaaaataggaacatttgagagatt 1012
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POR PRIMER'S
FORWARD: AGGAAACAGCTATGACCAT
BACKWARD: GTTTTCCCAGTCACGACG
Plate: 119 row: 0 column: 11
Seq primer: ATTTAGGTGACACTATAG.
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BF168710
601775935F1 NCI_CGAP_Lu29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Smith TPL USDA, ARS, US Meat Animal Research Center PO Box 166, Clay Center, NE 68933-0166, UT Tel: 402 762 4366 Fax: 402 762 4390 Email: smith@email.marc.usda.gov
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/db_xref="taxon:9823"
/clone_lib="MARC 1PIG"
/tissue_type="pooled"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: Xhc
Library made from pooled tissue from day 11, 13, 15,
and 30 embryos."
92 c 140 g 138 t
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92.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 460.8; DB 1
Pred. No. 1.2e-67;
0; Mismatches 42
            740 bp
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    musculus
              mRNA
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    CDNA
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COMMENT
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AUTHORS
TITLE
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Matches 597
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142 tgcgctggctgcgggacttcgcgctgcccaccgcgggcctgccaggacgcggagcagccga 201
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                                                                                          agtaccttaaagaccatgagaagaaaatgaaattggcatttaagagtttagacaaaaata 441
                                                                                                                                                                                                                                                                                                                                                                    GAGAGCTGCAGCAGGGGCTGCAAAGCCTGGGCATCCCGCTGGGCCAGGACGCGGAGGAGA 178
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                                                                                                                                                                                     AATACCTGAAAGACCATGAGAAGAAAATGAAATTAGCATTTAAAAAG-TTGGACAAGAATA
                                                                                                                                                                                                                                                                           AAATTTTCACCACTGGCGATGTCAACAAGATGGGAAGCTGGA-TTTGAAGAATTTATGA
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cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLN

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Plate: LLAM9266 row: f column:
High quality sequence stop: 668.
Location/Qualifiers
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1 (bases 1 to 740)
NIH-MCC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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BF168710
BF168710.1 GI:11049062
EST.
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Contact: Robert Strausberg, Ph.D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: cgapbs-r@mail.nih.gov
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Organ: lung; Vector: pCMV-SPORT6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo Library constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH"

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/tissue_type="spontaneous
Stem cell origin."
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/db_xref="taxon:10090"
/clone="IMAGE:4017416"
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Search completed: August 18, 2002, 07:16:47 Job time: 15484 sec

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